GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 16, 2003, 19:29:49 ; Search time 40 Seconds
(without alignments)
721.008 Million cell updates/sec

Title: US-09-935-727-2
Perfect score: 1634
Sequence: 1 MRALEGPGLSLLCLVLALPA.....RVARMPGLERSVRERFLPVH 300

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	351.5	21.5	461	1	A35356	tumor necrosis fac
2	333.5	20.4	459	2	I48854	gene murine tumour
3	332.5	20.3	474	2	B38634	tumor necrosis fac
4	315	19.3	435	2	I54182	tumor necrosis fac
5	295.5	18.1	651	2	JC7705	death receptor-6 -
6	262.5	16.1	349	2	D72175	G2R protein - vari
7	262.5	16.1	349	2	D36858	gene G4R protein -
8	262	16.0	348	2	T28623	hypothetical prote
9	236.5	14.5	325	2	B43692	T2 protein - rabbi
10	226	13.8	277	2	I37552	OX40 homolog - hum
11	215	13.2	326	1	GQVZML	T2 protein - myxom
12	214	13.1	271	2	S12783	OX40 antigen precu
13	211	12.9	277	2	A60771	B-cell activation
14	203	12.4	305	2	A46476	B cell-associated
15	198.5	12.1	272	2	I48700	gene ox40 protein
16	186.5	11.4	595	2	A42086	CD30 antigen precu
17	185	11.3	256	2	B32393	T-cell antigen 4-1
18	176	10.8	416	1	JN0006	nerve growth facto
19	175.5	10.7	427	1	GQHUN	nerve growth facto
20	174	10.6	255	2	I38426	lymphocyte activat
21	170	10.4	425	1	A26431	nerve growth facto
22	159.5	9.8	260	1	A46517	CD27 antigen precu
23	155.5	9.5	327	2	A46484	apoptosis-mediatin
24	148.5	9.1	1574	2	T13954	MEGF6 protein - ra
25	148	9.1	250	1	A49053	CD27 antigen precu
26	147.5	9.0	5376	2	T42215	zonadhesin - mouse
27	145	8.9	335	2	A40036	apoptosis-mediatin
28	144	8.8	324	2	JC2395	Fas antigen precur
29	143.5	8.8	1299	2	T43251	furin (EC 3.4.21.7
30	143	8.8	1620	2	T27283	hypothetical prote
31	140	8.6	314	2	I37383	FAS soluble protei
32	137.5	8.4	454	1	GQMST1	tumor necrosis fac
33	135	8.3	2321	2	S78549	notch3 protein - h
34	133	8.1	493	2	JC5486	membrane glycoprot
35	129.5	7.9	1548	2	S34583	serine proteinase
36	128.5	7.9	3635	2	T10053	laminin alpha 5 ch
37	127	7.8	1192	2	S69000	laminin gamma 2 ch
38	125.5	7.7	461	1	GQRTT1	tumor necrosis fac
39	125.5	7.7	1255	1	A24571	protein-tyrosine k
40	124.5	7.6	1713	2	A55347	adhesive ligand ep
41	124.5	7.6	3106	1	S53868	laminin alpha-2 ch
42	123.5	7.6	455	1	GQHUT1	tumor necrosis fac
43	122.5	7.5	2824	2	T22759	hypothetical prote
44	120	7.3	1609	1	MMHUB2	laminin gamma-1 ch
45	120	7.3	2318	2	S45306	notch 3 protein -

ALIGNMENTS

RESULT 1
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower,
Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular a
A;Reference number: A35356; MUID:90260639; PMID:2160731
A;Accession: A35356
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <SMI>
A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally oc
A;Reference number: A36475; MUID:91045991; PMID:2172983
A;Accession: A36475
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-195,'R',197-461 <KOH>
A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus,
Cytokine 2, 231-237, 1990
A;Title: Two human TNF receptors have similar extracellular, but distinct intracellul
A;Reference number: A48416; MUID:91370690; PMID:1966549
A;Accession: A48416
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 23-461 <DEM>
A;Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons
A;Reference number: A36007; MUID:90349572; PMID:2166946
A;Accession: A36007
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 116-140,'P',142-195,'R',197-362,'T',364-461 <HEL>
A;Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus,
J. Biol. Chem. 265, 20131-20138, 1990
A;Title: Purification and partial amino acid sequence analysis of two distinct tumor
A;Reference number: A23666; MUID:91056048; PMID:2173696
A;Accession: A23666
A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-40;65-69;136-141;300-306 <LOE>

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R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215; PMID:2153136
A;Accession: B35010
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-31 <ENG>
R;Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of
A;Reference number: I38094; MUID:95121934; PMID:7821811
A;Accession: I38094
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
C;Genetics:
A;Gene: GDB:TNFR2
A;Cross-references: GDB:125914; OMIM:191191
A;Map position: 1p36.2-1p36.2
A;Introns: 26/3
A;Note: the list of introns is incomplete
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;40-76/Domain: NGF receptor repeat homology <NG1>
F;78-119/Domain: NGF receptor repeat homology <NG2>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;164-201/Domain: NGF receptor repeat homology <NG4>
F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracellular #status predicted <INT>
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             21.5%;  Score 351.5;  DB 1;  Length 461;
  Best Local Similarity   29.8%;  Pred. No. 6.2e-19;
  Matches   96;  Conservative   43;  Mismatches  122;  Indels   61;  Gaps   12;

Qy          8 GLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGE-----------RLVCAQCPPG 55
              || |     ||||          || ||  |    | |             :: |::| ||
Db         13 GLELWAAAHALPA--------QVAFTPYAP----EPGSTCRLREYYDQTAQMCCSKCSPG 60

Qy         56 TFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRC 115
                :  | : | | |  |    ||| ||::  |  |   |   : | :||    || | |
Db         61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120

Qy        116 RTGFFAHAG------FCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQ 169
              | |::           |     | || ||  ||| : :  |:|| ||||| ::||:: |:
Db        121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180

Qy        170 PHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRL 229
              ||: |  :     :||::| | :||| :  |  :  |||    : |          :
Db        181 PHQICNVVA----IPGNASMDAVCTSTS--PTRSMAPGAVHLPQPV-------STRSQHT 227

Qy        230 QRLLQALEAPE-----GWGPTPRA----GRAALQLKLRRRLTELLGAQDGALLVRLLQAL 280
              |   :  ||        ||:| |    |  || : |   :| |     | |:: ::  :
Db        228 QPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTAL-----GLLIIGVVNCV 282

Qy        281 ---RVARMP-GLERSVRERFLP 298
                :| : |  |:|  :   ||
Db        283 IMTQVKKKPLCLQREAKVPHLP 304


RESULT 2
I48854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: I48854
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: I48854; MUID:95178848; PMID:7873884
A;Accession: I48854
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-459 <RES>
A;Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
F;151-188/Domain: NGF receptor repeat homology <NGF>

  Query Match             20.4%;  Score 333.5;  DB 2;  Length 459;
  Best Local Similarity   29.7%;  Pred. No. 1.4e-17;
  Matches   81;  Conservative   43;  Mismatches  110;  Indels   39;  Gaps    9;

Qy         46 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC 105
              :: ||:|||| :|:  | : | | |  |    ||| ||    | :|:  |   : | |||
Db         37 QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRAC 96

Qy        106 HATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 158
                  || | |  | :     |:|    |:  : | || || :   |: |  |: | ||||
Db         97 TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF 156

Qy        159 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPGAEECERA 214
              | ::||:: |:||| |: |     :||::| | :|     : :  | :  |   |
Db        157 SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQ 212

Qy        215 VIDFVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLTELLGAQD 269
                :|    |:    :   :| :|      | ||       |  :| : |   :| |
Db        213 PLD----QEPGPSQTPSILTSL------GSTPIIEQSTKGGISLPIGLIVGVTSL----- 257

Qy        270 GALLVRLLQAL----RVARMPGLERSVRERFLP 298
              | |:: |:       |  :   |:|  :   :|
Db        258 GLLMLGLVNCFILVQRKKKPSCLQRDAKVPHVP 290


RESULT 3
B38634
tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
A;Reference number: A38634; MUID:91187885; PMID:1849278
A;Accession: B38634
A;Molecule type: mRNA
A;Residues: 1-474 <LEW>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A;Reference number: A40254; MUID:91246168; PMID:1645445
A;Accession: A40254
A;Molecule type: mRNA
A;Residues: 1-474 <GOO>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
submitted to the EMBL Data Library, May 1995
A;Description: Characterization of the promoter region of the murine p75-TNF receptor
A;Reference number: S54816
A;Accession: S54816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <KIS>
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
C;Keywords: cytokine receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F;40-77/Domain: NGF receptor repeat homology <NG1>
F;79-120/Domain: NGF receptor repeat homology <NG2>
F;166-203/Domain: NGF receptor repeat homology <NG4>
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  Query Match            20.3%;  Score 332.5;  DB 2;  Length 474;
  Best Local Similarity  29.7%;  Pred. No. 1.7e-17;
  Matches   81;  Conservative   44;  Mismatches  109;  Indels   39;  Gaps    9;

Qy         46 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC 105
              :: ||:|||| :|:  | : | | |  |    ||| ||    |  |:  |   : | |||
Db         52 QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRAC 111

Qy        106 HATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 158
                || | |  | :     |:|    |:  : | || || :   |: |  |: | ||||
Db        112 TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF 171

Qy        159 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPGAEECERA 214
              | ::||:: |:||| |: |     :||::| | :|     : :  | :  |   |
Db        172 SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQ 227

Qy        215 VIDFVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLTELLGAQD 269
               :|    |:    :  :| :|      | ||       |  :| : |  . :| |
Db        228 PLD----QEPGPSQTPSILTSL------GSTPIIEQSTKGGISLPIGLIVGVTSL----- 272

Qy        270 GALLVRLLQAL----RVARMPGLERSVRERFLP 298
              | |:: |:  :    |  :   |:|  :   :|
Db        273 GLLMLGLVNCIILVQRKKKPSCLQRDAKVPHVP 305


RESULT 4
I54182
tumor necrosis factor receptor 2-related protein - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C;Accession: I54182
R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A;Reference number: I54182; MUID:93252381; PMID:8486360
A;Accession: I54182
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-435 <RES>
A;Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C;Genetics:
A;Gene: GDB:LTBR
A;Cross-references: GDB:1230195; OMIM:600979
A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

  Query Match            19.3%;  Score 315;  DB 2;  Length 435;
  Best Local Similarity  31.8%;  Pred. No. 3.1e-16;
  Matches   89;  Conservative   29;  Mismatches  120;  Indels   42;  Gaps   12;

Qy          3 ALEGPGLSLLCLVLALPALLPVPAVRGVAETPTY-----PWRDA-----ETGERLVCAQC 52
              |   |||:   ||| |  ||      : |   | |         ||       |   |: |::|
Db          6 ATSAPGLAWGPLVLGLFGLLAASQPQAV---PPYASENQTCRDQEKEYYEPQHRICCSRC 62

Qy         53 PPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYL---ERCRYCNVLCGEREEEARACHATH 109
              ||||:|   | |   | | |    | : ||||    : || |: : |   ||   | :
Db         63 PPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMG--LEEIAPCTSKR 120

Qy        110 NRACRCRTGFFAHAGFCLE--H----ASCPPGA-GVIAPGTPSQNTQCQPCPPGTFSASS 162
                 |||: | |  | : ||  |    : ||||    :         |  | ||  | |  :|
Db        121 KTQCRCQPGMFC-AAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHFQNTS 179

Qy        163 SSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQ 222
              | | :|||| |   ||    ||::  || | :    ||   : |       ::    |
Db        180 SPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLE-PLPPEMSGTMLMLAVLLPLAFFL 238

Qy        223 DIS------------IKRLQRLLQALEAPEGWGPTPRAG 249
               ::              ::|  ||:    |:| || | ||
Db        239 LLATVFSCIWKSHPSLCRKLGSLLK--RRPQGEGPNPVAG 276


RESULT 5
JC7705
death receptor-6 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: JC7705
R;Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A;Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A;Reference number: JC7705; MUID:21308433; PMID:11414698
A;Accession: JC7705
A;Molecule type: mRNA
A;Residues: 1-651 <BRI>
A;Cross-references: GB:AF349908
C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belo
tresia, activates a cell death and/or survival signaling cascade.
C;Genetics:
A;Gene: dr-6
C;Keywords: ovary
F;1-21/Domain: signal sequence #status predicted <SIG>
F;52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F;332-350/Domain: transmembrane #status predicted <TMM>
F;410-475/Domain: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted

  Query Match            18.1%;  Score 295.5;  DB 2;  Length 651;
  Best Local Similarity  30.8%;  Pred. No. 1.3e-14;
  Matches   61;  Conservative   30;  Mismatches   92;  Indels   15;  Gaps    1;

Qy         18 LPALLPVPAVRGVAETP--------------TYPWRDAETGERLVCAQCPPGTFVQRPC 62
              | |:||:    | |:                  |   |  | : |:| :|| ||:| : |
Db          6 LAAVLPLLVFLGTADAQPKLTSEQNAVSLPAGKYLHLDRATNQELICDKCPAGTYVSKHC 65

Qy         63 RRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAH 122
               : :   | |||   :|:  | :|||  |   |      |   | |  :| | | :| |
Db         66 TKSTLRECSPCPDGTFTKHENGIERCHPCRKPCELPMIEKTHCTALTDRECTCLSGTFQI 125

Qy        123 AGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALN 182
               |: :  || | ||   || ::: :|:||  ||||   ||  :|: : :|    : :
Db        126 NDTCVPYTVCPVGWGVRKKGTETEDVRCKPCLRGTFSDVPSSVMKCKTYTDCFGKNMVVV 185

Qy        183 VPGSSSHDTLCTSCTGFP 200
              ||:   | :| |    |
Db        186 KPGTKESDNVCXSPASLP 203


RESULT 6
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C;Accession: D72175
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lo
submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola mi
A;Reference number: A72150
A;Accession: D72175
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <SHC>
A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A;Experimental source: strain Garcia-1966
C;Genetics:
A;Gene: G2R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

  Query Match            16.1%;  Score 262.5;  DB 2;  Length 349;
  Best Local Similarity  30.0%;  Pred. No. 2.1e-12;
  Matches   62;  Conservative   29;  Mismatches  103;  Indels   13;  Gaps    3;

Qy          9 LSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPT 68
              | | |:::      |     |  :   |          | |  |||||:  | |   : |
Db         10 LFLSCIIINGRDAAPYTPPNGKCKDTEY------KRHNLCCLSCPPGTYASRLCDSKTNT 63

Qy         69 TCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF------AH 122
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Db         64 QCTPCGSGTFTSRNNHLPACLSCNGRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSG 123

Qy        123 AGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALN 182

Db        124 CKACVSQTKCGIGYGV-SGHTSVGDVICSPCGFGTYSYTVSSTDKCEPVPNNTFNYIDVE 182

Qy        183 VPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Db        183 ITLYPVNDTSCTRTTTTGLSESILTSE 209


RESULT 7
D36858
gene G4R protein - variola virus
N;Alternate names: B28R protein (COP)
C;Species: variola virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C;Accession: D36858; S46888; S32385; S35987
R;Blinov, V.M.
submitted to GenBank, November 1992
A;Reference number: A36859
A;Accession: D36858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <BLI>
A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
R;Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frol
submitted to the EMBL Data Library, April 1992
A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
A;Reference number: S46868
A;Accession: S46888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <KOL>
A;Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A;Experimental source: strain India-1967, isolate Ind3
R;Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A;Reference number: S32385; MUID:93202281; PMID:8384129
A;Accession: S32385
A;Molecule type: DNA
A;Residues: 31-168 <SHC>
A;Cross-references: EMBL:X69198
A;Experimental source: strain India-1967, ssp. major
C;Genetics:
A;Gene: G4R
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;32-66/Domain: NGF receptor repeat homology <NGF>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-151/Domain: NGF receptor repeat homology <NG3>

  Query Match             16.1%;  Score 262.5;  DB 2;  Length 349;
  Best Local Similarity   30.0%;  Pred. No. 2.1e-12;
  Matches   62;  Conservative   29;  Mismatches  103;  Indels   13;  Gaps    3;

Qy          9 LSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPT 68

Db         10 LFLSCIIINGRDAAPYTPPNGKCKDTEY------KRHNLCCLSCPPGTYASRLCDSKTNT 63

Qy         69 TCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF------AH 122

Db         64 QCTPCGSGTFTSRNNHLPACLSCNGRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSG 123

Qy        123 AGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALN 182

Db        124 CKACVSQTKCGIGYGV-SGHTSVGDVICSPCGFGTYSHTVSSADKCEPVPNNTFNYIDVE 182

Qy        183 VPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Db        183 ITLYPVNDTSCTRTTTTGLSESILTSE 209


RESULT 8
T28623
hypothetical protein G2R - variola major virus
C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T28623
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Au
Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox vir
A;Reference number: Z20488; MUID:94088747; PMID:8264798
A;Accession: T28623
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-348 <MAS>
A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A;Experimental source: strain Bangladesh 1975
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

  Query Match             16.0%;  Score 262;  DB 2;  Length 348;
  Best Local Similarity   30.8%;  Pred. No. 2.3e-12;
  Matches   64;  Conservative   28;  Mismatches  100;  Indels   16;  Gaps    4;

Qy          9 LSLLCLVLALPALLPVPAVRGVAETPTYPWRDAE-TGERLVCAQCPPGTFVQRPCRRDSP 67

Db         10 LFLSCIINGRDAAPYTP--------PNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTN 61

Qy         68 TTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF------A 121

Db         62 TQCTPCGSGTFTSRNNHLPACLSCNGRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSS 121

Qy        122 HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLAL 181

Db        122 GCKACVSQTKCGIGYGV-SGHTSVGDVICSPCGFGTYSHTVSSADKCEPVPNNTFNYIDV 180

Qy        182 NVPGSSSHDTLCTSCTGFPLSTRVPGAE 209

Db        181 EITLYPVNDTSCTRTTTTGLSESILTSE 208


RESULT 9
B43692
T2 protein - rabbit fibroma virus
C;Species: rabbit fibroma virus, Shope fibroma virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: B43692
R;Upton, C.; DeLange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A;Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomer
A;Reference number: A43692; MUID:87321103; PMID:2820128
A;Accession: B43692
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-325 <UPT>
A;Cross-references: GB:M17433
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>

  Query Match             14.5%;  Score 236.5;  DB 2;  Length 325;
  Best Local Similarity   29.9%;  Pred. No. 1.7e-10;
  Matches   58;  Conservative   25;  Mismatches   94;  Indels   17;  Gaps    4;

Qy         11 LLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTC 70

Db          8 LVCVVYVYGDDVPYSSNQGKCGGHDY------EKDGLCCASCHPGFYASRLCGPGSNTVC 61

Qy         71 GPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFFA------HAG 124

Db         62 SPCEDGTFTASTNHAPACVSCRGPCTGHLSESQPCDRTHDRVCNCSTGNYCLLKGQNGCR 121

Qy        125 FCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVP 184
```

```
Db        122 ICAPQTKCPAGYGV-SGHTRAGDTLCEKCPPHTYSDSLSPTERCGTSFNYISVGFNL--- 177

Qy        185 GSSSHDTLCTSCTG 198
Db        178 -YPVNETSCTTTAG 190
```

RESULT 10
I37552
OX40 homolog - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C;Accession: I37552
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat
Eur. J. Immunol. 24, 677-683, 1994
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment c
A;Reference number: I37552; MUID:94170844; PMID:7510240
A;Accession: I37552
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <RES>
A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g472958
C;Superfamily: CD27 antigen; NGF receptor repeat homology

  Query Match 13.8%; Score 226; DB 2; Length 277;
  Best Local Similarity 27.0%; Pred. No. 8.9e-10;
  Matches 80; Conservative 25; Mismatches 117; Indels 74; Gaps 12;

```
Qy          6 GPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRD 65
Db         11 GPCAALLLLGLGLSTVTGLHCV-----GDTYPSNDR------CCHECRPGNGMVSRCSRS 59

Qy         66 SPTTCGPCPPRHYTQFWNY--LERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHA 123
Db         60 QNTVCRPCGPGFYNDVVSSKPCKPCTWCNLRSG--SERKQLCTATQDTVCRCRAG----- 112

Qy        124 GFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNV 183
Db        113 --TQPLDSYKPG-----------VDCAPCPPGHF--SPGDNQACKPWTNCTLAGKHTLQ 156

Qy        184 PGSSSHDTLCTS---CTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
Db        157 PASNSSDAICEDRDPPATQPQETQGPPARPI----------TVQPTE 193

Qy        241 GW-----GPTPR-----AGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMP 286
Db        194 AWPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPL--AILLALYLLRRDQRLP 247
```

RESULT 11
GQVZML
T2 protein - myxoma virus (strain Lausanne)
C;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: A40566
R;Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991
A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis f
A;Reference number: A40566; MUID:91335768; PMID:1651597
A;Accession: A40566
A;Molecule type: DNA
A;Residues: 1-326 <UPT>
A;Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C;Keywords: glycoprotein
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
F;66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match 13.2%; Score 215; DB 1; Length 326;
  Best Local Similarity 29.3%; Pred. No. 6.9e-09;
  Matches 58; Conservative 22; Mismatches 96; Indels 22; Gaps 5;

```
Qy         12 LCLVLALPALL-----PVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDS 66
Db          4 LTLLLAYVACVYGGGAPYGADRGKCRGNDY------EKDGLCCTSCPPGSYASRLCGPGS 57

Qy         67 PTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFFA----- 121
Db         58 DTVCSPCKNETFTASTNHAPACVSCRGRCTGHLSESQSCDKTRDRVCDCSAGNYCLLKGQ 117

Qy        122 -HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
Db        118 EGCRICAPKTKCPAGYGV-SGHTRTGDVLCTKCPRYTYSDAVSSTETCTSSFNYISVEFN 176

Qy        181 LNVPGSSSHDTLCTSCTG 198
Db        177 L----YPVNDTSCTTTAG 190
```

RESULT 12
S12783
OX40 antigen precursor - rat
N;Alternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C;Accession: S12783; S08036
R;Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc
A;Reference number: S12783; MUID:90214614; PMID:2157591
A;Accession: S12783
A;Molecule type: mRNA
A;Residues: 1-271 <MAL>
A;Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-271/Product: OX40 antigen #status predicted <MAT>
F;211-235/Domain: transmembrane #status predicted <TMM>

  Query Match 13.1%; Score 214; DB 2; Length 271;
  Best Local Similarity 30.1%; Pred. No. 6.9e-09;
  Matches 58; Conservative 23; Mismatches 64; Indels 48; Gaps 9;

```
Qy         10 SLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTT 69
Db         10 AFLLLGLSLGVTVKLNCVK-----DTYP-----SGHK-CCRECQPGHGMVSRCDHTRDTV 58

Qy         70 CGPCPPRHYTQFWNY--LERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCL 127
Db         59 CHPCEPGFYNEAVNYDTCKQCTQCNHRSG--SELKQNCTPTEDTVCQCR---------- 105

Qy        128 EHASCPPGAGVIAPGT-PSQNT------QCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
Db        106 -------------PGTQPRQDSSHKLGVDCVPCPPGHF--SPGSNQACKPWTNCTLSGKQ 150

Qy        181 LNVPGSSSHDTLC 193
Db        151 IRHPASNSLDTVC 163
```

RESULT 13
A60771
B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: S04460; A60771
R;Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor recept
A;Reference number: S04460; MUID:89356608; PMID:2475341
A;Accession: S04460
A;Molecule type: mRNA

```
A;Residues: 1-277 <STA>
A;Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-lik
A;Reference number: A60771; MUID:89093941; PMID:2463309
A;Accession: A60771
A;Molecule type: protein
A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line Raji
C;Genetics:
A;Gene: GDB:CD40
A;Cross-references: GDB:215268; OMIM:109535
A;Map position: 20q12-20q13.2
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-193/Domain: extracellular #status predicted <EXT>
F;194-215/Domain: transmembrane #status predicted <TMM>
F;216-277/Domain: intracellular #status predicted <CYT>
F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             12.9%;  Score 211;  DB 2;  Length 277;
  Best Local Similarity   30.5%;  Pred. No. 1.2e-08;
  Matches   46;  Conservative   21;  Mismatches   76;  Indels    8;  Gaps    3;

Qy          49 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERC---RYCNVLCGEREEEARAC 105
               |: | ||  :   |   : | | ||    :   ||   |   :||:   | | ::
Db          38 CSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTS 97

Qy         106 HATHNRACRCRTGFFAHA---GFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASS 162
                 :  | |   |:    :     |: | || || ||    |   :| |:|||  | ||  |
Db          98 ET--DTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVS 155

Qy         163 SSSEQCQPHRNCTALGLALNVPGSSSHDTLC 193
               |: |:| |  :|    | :   |::  | :|
Db         156 SAFEKCHPWTSCETKDLVVQQAGTNKTDVVC 186


RESULT 14
A46476
B cell-associated surface molecule CD40, long splice form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Accession: A46476; A46515
R;Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A;Reference number: A46476; MUID:92105763; PMID:1370315
A;Accession: A46476
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-305 <TOR>
A;Cross-references: GB:M83312; NID:g1553058
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,
J. Immunol. 149, 3921-3926, 1992
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A;Reference number: A46515; MUID:93094586; PMID:1281194
A;Accession: A46515
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-287,'LV' <GRI>
A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; N
A;Experimental source: BALB/c, liver
A;Note: sequence extracted from NCBI backbone (NCBIP:120357)
C;Comment: For an alternative splice form, see PIR:A46515.
C;Comment: For an alternative splice form, see PIR:A46476.
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology <NGF>

  Query Match             12.4%;  Score 203;  DB 2;  Length 305;
  Best Local Similarity   31.1%;  Pred. No. 5.1e-08;
  Matches   47;  Conservative   19;  Mismatches   77;  Indels    8;  Gaps    3;

Qy          49 CAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERC---RYCNVLCGEREEEARAC 105
               |  | ||: :   |     | | ||    ::  ||   ||   |:|    | | ::
Db          38 CDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCEPNQGLRVKKEGT- 96

Qy         106 HATHNRACRCRTGFFA---HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASS 162
                 |  :  | |: |          | :|  | || ||:   | : :| | ||| | ||  |
Db          97 -AESDTVCTCKEGQHCTSKDCEACAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQS 155

Qy         163 SSSEQCQPHRNCTALGLALNVPGSSSHDTLC 193
               |  |:| |  :|    | :   |:|  : :|
Db         156 SLFEKCYPWTSCEDKNLEVLQKGTSQTNVIC 186


RESULT 15
I48700
gene ox40 protein - mouse
N;Alternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: I48700; I48334; S34377
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J
J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell
A;Reference number: I48700; MUID:94044750; PMID:8228223
A;Accession: I48700
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-272 <RES>
A;Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A;Title: Gene structure and chromosomal localization of the mouse homologue of rat OX
A;Reference number: I48334; MUID:95255413; PMID:7737295
A;Accession: I48334
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-14,'G',16-272 <RE2>
A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C;Genetics:
A;Gene: ox40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology

  Query Match             12.1%;  Score 198.5;  DB 2;  Length 272;
  Best Local Similarity   30.3%;  Pred. No. 9.9e-08;
  Matches   57;  Conservative   17;  Mismatches   71;  Indels   43;  Gaps    8;

Qy          15 VLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCP 74
               :| |   | | | |      |||     :| :  | :| ||  :   |     | | ||
Db          11 LLLLALTLGVTARRLNCVKHTYP-----SGHK-CCRECQPGHGMVSRCDHTRDTLCHPCE 64

Qy          75 PRHYTQFWNY--LERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASC 132
                   | :  ||   ::|  ||   |   |  : |  | :  ||||
Db          65 TGFYNEAVNYDTCKQCTQCNHRSG--SELKQNCTPTQDTVCRCR---------------- 106

Qy         133 PPGAGVIAPGT-PSQNT------QCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPG 185
                    ||| | |::       | ||||| |  |  ::: |:|  |||  |     |
Db         107 --------PGTQPRQDSGYKLGVDCVPCPPGHF--SPGNNQACKPWTNCTLSGKQTRHPA 156

Qy         186 SSSHDTLC 193
               | | | :|
Db         157 SDSLDAVC 164


Search completed: July 16, 2003, 19:39:45
Job time : 41 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 16, 2003, 19:39:49 ; Search time 19 Seconds
(without alignments)
1517.912 Million cell updates/sec

Title: US-09-935-727-2
Perfect score: 300
Sequence: 1 MRALEGPGLSLLCLVLALPA.....RVARMPGLERSVRERFLPVH 300

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9	3.0	327	2	H83483	probable transmemb
2	9	3.0	561	2	D84800	hypothetical prote
3	8	2.7	179	1	KGRT	gamma-casein precu
4	8	2.7	181	2	T49104	hypothetical prote
5	8	2.7	184	2	I49685	gamma-casein precu
6	8	2.7	191	2	G90670	probable oxidoredu
7	8	2.7	191	2	C85521	probable oxidoredu
8	8	2.7	241	2	T05479	hypothetical prote
9	8	2.7	297	2	AH0341	probable aldo/keto
10	8	2.7	341	2	T27654	hypothetical prote
11	8	2.7	440	2	T50912	hypothetical prote
12	8	2.7	494	1	S60028	ferredoxin-NADP re
13	8	2.7	494	2	AD0751	cytoplasmic alpha-
14	8	2.7	530	2	F90893	probable kinase [i
15	8	2.7	530	2	C85724	probable kinase yd
16	8	2.7	530	2	B64905	sugar kinase homol
17	8	2.7	531	1	S54098	1-phosphatidylinos
18	8	2.7	644	2	JC5119	anti-mullerian hor
19	8	2.7	781	2	T49472	hormone-sensitive
20	8	2.7	1172	1	TSHUP2	thrombospondin 2 p
21	7	2.3	26	1	B57082	secretin - guinea
22	7	2.3	27	1	S07443	secretin - human
23	7	2.3	27	1	SEBO	secretin - bovine
24	7	2.3	27	1	SESH	secretin - sheep
25	7	2.3	27	2	A27267	secretin - dog
26	7	2.3	27	2	C60415	secretin - rabbit
27	7	2.3	56	2	A95955	hypothetical expor
28	7	2.3	57	2	C84255	hypothetical prote
29	7	2.3	74	2	S13515	retinoic acid rece
30	7	2.3	87	2	G85063	hypothetical prote
31	7	2.3	89	2	S13517	retinoic acid rece
32	7	2.3	106	2	G82729	hypothetical prote
33	7	2.3	112	2	G72502	hypothetical prote
34	7	2.3	113	1	IMECE1	colicin E1 immunit
35	7	2.3	113	2	I64785	imm protein - Esch
36	7	2.3	113	2	S11532	colicin E1 immunit
37	7	2.3	114	2	S44660	ZK353.5 protein -
38	7	2.3	118	2	S27476	hypothetical prote
39	7	2.3	131	1	SEPG	secretin precursor
40	7	2.3	133	2	JC2202	secretin precursor
41	7	2.3	134	2	A40959	secretin precursor
42	7	2.3	140	2	T27059	hypothetical prote
43	7	2.3	140	2	C72705	hypothetical prote
44	7	2.3	144	1	TVVPBD	small T antigen -
45	7	2.3	150	2	S34380	hypothetical prote

ALIGNMENTS

RESULT 1
H83483
probable transmembrane sensor PA1301 [imported] - Pseudomonas aeruginosa (strain PAO1
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Jun-2001
C;Accession: H83483
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83483
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-327 <STO>
A;Cross-references: GB:AE004559; GB:AE004091; NID:g9947228; PIDN:AAG04690.1; GSPDB:GN
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1301
C;Superfamily: Pseudomonas putida regulatory protein pupR

Query Match 3.0%; Score 9; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         16 LALPALLPV 24
              |||||||||
Db        304 LALPALLPV 312
```

RESULT 2
D84800
hypothetical protein At2g38060 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: D84800
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84800
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-561 <STO>
A;Cross-references: GB:AE002093; NID:g4895179; PIDN:AAD32766.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g38060
A;Map position: 2

Query Match 3.0%; Score 9; DB 2; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 GPGLSLLCL 14
              |||||||||
Db        405 GPGLSLLCL 413
```

RESULT 3
KGRT
gamma-casein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 31-May-1996
C;Accession: A03111
R;Hobbs, A.A.; Rosen, J.M.
Nucleic Acids Res. 10, 8079-8098, 1982
A;Title: Sequence of rat alpha- and gamma-casein mRNAs: evolutionary comparison of the c
A;Reference number: A93452; MUID:83143278; PMID:6298707
A;Accession: A03111
A;Molecule type: mRNA
A;Residues: 1-179 <HOB>
C;Superfamily: gamma-casein
C;Keywords: phosphoprotein
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-179/Product: gamma-casein #status predicted <MAT>

Query Match 2.7%; Score 8; DB 1; Length 179;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        159 SASSSSSE 166
              ||||||||
Db         50 SASSSSSE 57
```

RESULT 4
T49104
hypothetical protein AT4g21970 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49104
R;Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; M
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25016
A;Accession: T49104
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-181 <BEV>
A;Cross-references: EMBL:AL022140; GSPDB:GN00062; ATSP:AT4g21970
A;Experimental source: cultivar Columbia; BAC clone F1N20
C;Genetics:
A;Gene: ATSP:AT4g21970
A;Map position: 4
A;Introns: 142/1

Query Match 2.7%; Score 8; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        158 FSASSSSS 165
              ||||||||
Db         35 FSASSSSS 42
```

RESULT 5
I49685
gamma-casein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 13-Aug-1999
C;Accession: I49685
R;Sasaki, T.; Sasaki, M.; Enami, J.
Zool. Sci. 10, 65-72, 1993
A;Title: Mouse gamma-casein cDNA: PCR cloning and sequence analysis.
A;Reference number: I49685; MUID:93320737; PMID:7763793
A;Accession: I49685
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-184 <RES>
A;Cross-references: GB:D10215; NID:g220404; PIDN:BAA01067.1; PID:g220405
C;Superfamily: gamma-casein

Query Match 2.7%; Score 8; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        159 SASSSSSE 166
              ||||||||
Db         51 SASSSSSE 58
```

RESULT 6
G90670
probable oxidoreductase ECs0335 [imported] - Escherichia coli (strain O157:H7, substr
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: G90670
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G90670
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-191 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33758.1; PID:g13359792; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0335

Query Match 2.7%; Score 8; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        210 ECERAVID 217
              ||||||||
Db         27 ECERAVID 34
```

RESULT 7
C85521
probable oxidoreductase ECs0335 [imported] - Escherichia coli (strain O157:H7, substr
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C;Accession: C85521
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: C85521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-191 <STO>
A;Cross-references: GB:AE005174; NID:g12513095; PIDN:AAG54631.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0374

Query Match 2.7%; Score 8; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        210 ECERAVID 217
              ||||||||
```

```
Db         27 ECERAVID 34


RESULT 8
T05479
hypothetical protein T8O5.180 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C;Accession: T05479
R;Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuelle
submitted to the Protein Sequence Database, February 1998
A;Reference number: Z15417
A;Accession: T05479
A;Molecule type: DNA
A;Residues: 1-241 <BEV>
A;Cross-references: EMBL:AL021890
A;Experimental source: cultivar Columbia; BAC clone T8O5
C;Genetics:
A;Map position: 4
A;Introns: 142/1; 169/3; 193/1; 211/1; 223/3
A;Note: T8O5.180

  Query Match             2.7%;  Score 8;  DB 2;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        158 FSASSSSS 165
              ||||||||
Db         35 FSASSSSS 42


RESULT 9
AH0341
probable aldo/keto reductase (EC 1.1.1.-) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AH0341
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0341
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-297 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC93039.1; PID:g15980777; GSPDB:GN00175
C;Genetics:
A;Gene: YPO2805
C;Superfamily: aldehyde reductase
C;Keywords: oxidoreductase

  Query Match             2.7%;  Score 8;  DB 2;  Length 297;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        210 ECERAVID 217
              ||||||||
Db         41 ECERAVID 48


RESULT 10
T27654
hypothetical protein ZK1025.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27654
R;Lennard, N.
submitted to the EMBL Data Library, March 1998
A;Reference number: Z20400
A;Accession: T27654
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-341 <WIL>
A;Cross-references: EMBL:AL022288; PIDN:CAA18368.1; GSPDB:GN00019; CESP:ZK1025.9
A;Experimental source: clone ZK1025
C;Genetics:
A;Gene: CESP:ZK1025.9
A;Map position: 1
A;Introns: 6/1; 54/1; 76/1; 97/1; 158/3; 232/2; 324/3

  Query Match             2.7%;  Score 8;  DB 2;  Length 341;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        159 SASSSSSE 166
              ||||||||
Db        103 SASSSSSE 110


RESULT 11
T50912
hypothetical protein ORF440 [imported] - Rubrivivax gelatinosus
C;Species: Rubrivivax gelatinosus
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C;Accession: T50912
R;Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.
submitted to the EMBL Data Library, November 1999
A;Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photos
A;Reference number: Z25270
A;Accession: T50912
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-440 <NAG>
A;Cross-references: EMBL:AB034704; PIDN:BAA94065.1
A;Experimental source: strain IL144
C;Genetics:
A;Note: ORF440

  Query Match             2.7%;  Score 8;  DB 2;  Length 440;
  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 LALPALLP 23
              ||||||||
Db         42 LALPALLP 49


RESULT 12
S60028
ferredoxin-NADP reductase (EC 1.18.1.2) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C;Accession: S60028; I49671
R;Itoh, S.; Iemura, O.; Yamada, E.; Yoshimura, T.; Tsujikawa, K.; Kohama, Y.; Mimura,
Biochim. Biophys. Acta 1264, 159-162, 1995
A;Title: cDNA cloning of mouse ferredoxin reductase from kidney.
A;Reference number: I49671; MUID:96085117; PMID:7495857
A;Accession: S60028
A;Molecule type: mRNA
A;Residues: 1-494 <ITO>
A;Cross-references: EMBL:D49920; NID:g1088468; PIDN:BAA08659.1; PID:g1088469
C;Genetics:
A;Genome: nuclear
C;Superfamily: human ferredoxin-NADP+ reductase
C;Keywords: FAD; mitochondrion; NADP; oxidoreductase
F;1-34/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;35-494/Product: ferredoxin-NADP+ reductase #status predicted <MAT>

  Query Match             2.7%;  Score 8;  DB 1;  Length 494;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        258 RRRLTELL 265
              ||||||||
```

```
Db        276 RRRLTELL 283


RESULT 13
AD0751
cytoplasmic alpha-amylase [imported] - Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: AD0751
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AD0751
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-494 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05711.1; PID:g16503204; GSPDB:GN00176
C;Genetics:
A;Gene: STY2171
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

  Query Match             2.7%;  Score 8;  DB 2;  Length 494;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        232 LLQALEAP 239
              ||||||||
Db        335 LLQALEAP 342


RESULT 14
F90893
probable kinase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 24-Aug-2001
C;Accession: F90893
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90893
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-530 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB35541.1; PID:g13361584; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs2118
C;Superfamily: xylulokinase

  Query Match             2.7%;  Score 8;  DB 2;  Length 530;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         41 AETGERLV 48
              ||||||||
Db        475 AETGERLV 482


RESULT 15
C85724
probable kinase ydeV [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: C85724
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: C85724
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-530 <STO>
A;Cross-references: GB:AE005174; NID:g12515155; PIDN:AAG56255.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: ydeV
C;Superfamily: xylulokinase

  Query Match             2.7%;  Score 8;  DB 2;  Length 530;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         41 AETGERLV 48
              ||||||||
Db        475 AETGERLV 482


Search completed: July 16, 2003, 19:42:25
Job time : 21 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 16, 2003, 19:26:08 ; Search time 23 Seconds
(without alignments)
540.996 Million cell updates/sec

Title: US-09-935-727-2
Perfect score: 1634
Sequence: 1 MRALEGPGLSLLCLVLALPA.....RVARMPGLERSVRERFLPVH 300

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1634	100.0	300	1	TR6B_HUMAN	O95407 homo sapien
2	444	27.2	401	1	T11B_HUMAN	O00300 homo sapien
3	425.5	26.0	401	1	T11B_RAT	O08727 rattus norv
4	424.5	26.0	401	1	T11B_MOUSE	O08712 mus musculu
5	351.5	21.5	461	1	TR1B_HUMAN	P20333 homo sapien
6	332.5	20.3	474	1	TR1B_MOUSE	P25119 mus musculu
7	315	19.3	435	1	TNR3_HUMAN	P36941 homo sapien
8	291.5	17.8	655	1	TR21_MOUSE	Q9epu5 mus musculu
9	287	17.6	655	1	TR21_HUMAN	O75509 homo sapien
10	277	17.0	415	1	TNR3_MOUSE	P50284 mus musculu
11	262.5	16.1	349	1	CRMB_VARV	P34015 variola vir
12	261.5	16.0	349	1	CRMB_CAMPS	Q8uya7 camelpox vi
13	258.5	15.8	351	1	CRMB_COWPX	O73559 cowpox viru
14	246	15.1	283	1	TR14_HUMAN	Q92956 homo sapien
15	239	14.6	616	1	TR11_HUMAN	Q9y6q6 homo sapien
16	236.5	14.5	325	1	VT2_SFVKA	P25943 shope fibro
17	233.5	14.3	625	1	TR11_MOUSE	O35305 mus musculu
18	226	13.8	277	1	TNR4_HUMAN	P43489 homo sapien
19	215	13.2	326	1	VT2_MYXVL	P29825 myxoma viru
20	214	13.1	271	1	TNR4_RAT	P15725 rattus norv
21	211	12.9	277	1	TNR5_HUMAN	P25942 homo sapien
22	203	12.4	289	1	TNR5_MOUSE	P27512 mus musculu
23	202	12.4	269	1	TNR5_BOVIN	Q28203 bos taurus
24	198.5	12.1	272	1	TNR4_MOUSE	P47741 mus musculu
25	186.5	11.4	595	1	TNR8_HUMAN	P28908 homo sapien
26	185	11.3	256	1	TNR9_MOUSE	P20334 mus musculu
27	182.5	11.2	180	1	TR22_MOUSE	Q9er62 mus musculu
28	176	10.8	416	1	TR16_CHICK	P18519 gallus gall
29	175.5	10.7	427	1	TR16_HUMAN	P08138 homo sapien
30	174	10.6	255	1	TNR9_HUMAN	Q07011 homo sapien
31	170	10.4	425	1	TR16_RAT	P07174 rattus norv
32	167.5	10.3	176	1	TR23_MOUSE	Q9er63 mus musculu
33	166	10.2	417	1	TR16_MOUSE	Q9z0w1 mus musculu
34	163	10.0	332	1	TNR6_PIG	O77736 sus scrofa
35	160.5	9.8	471	1	TR1A_BOVIN	O19131 bos taurus
36	155.5	9.5	260	1	TNR7_HUMAN	P26842 homo sapien
37	155.5	9.5	327	1	TNR6_MOUSE	P25446 mus musculu
38	155	9.5	323	1	TNR6_BOVIN	P51867 bos taurus
39	153	9.4	241	1	TR18_HUMAN	Q9y5u5 homo sapien
40	152.5	9.3	430	1	TRLT_MACFA	Q9n092 macaca fasc
41	151.5	9.3	430	1	TRLT_HUMAN	Q969z4 homo sapien
42	148	9.1	250	1	TNR7_MOUSE	P41272 mus musculu
43	147.5	9.0	5376	1	ZAN_MOUSE	O88799 mus musculu
44	147	9.0	1581	1	LMG3_MOUSE	Q9r0b6 mus musculu
45	145	8.9	335	1	TNR6_HUMAN	P25445 homo sapien

ALIGNMENTS

RESULT 1
TR6B_HUMAN
ID TR6B_HUMAN STANDARD; PRT; 300 AA.
AC O95407;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
DE receptor for Fas ligand) (Decoy receptor 3) (DcR3) (M68).
GN TNFRSF6B OR DCR3 OR TR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal lung;
RX MEDLINE=99087326; PubMed=9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Botstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
RC TISSUE=Prostate;
RX MEDLINE=99253915; PubMed=10318773;
RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20122600; PubMed=10655513;
RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M68/DcR3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Decoy receptor for the cytotoxic ligands TNFS14/LIGHT
CC and TNFSF6/FasL. Protects against apoptosis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.

```
CC       Detected in adult stomach, spinal cord, lymph node, trachea,
CC       spleen, colon and lung. Highly expressed in several primary tumors
CC       from colon, stomach, rectum, esophagus and in SW480 colon
CC       carcinoma cells.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF104419; AAD03056.1; -.
DR   EMBL; AF134240; AAD29688.1; -.
DR   EMBL; AF217796; AAF35244.1; -.
DR   EMBL; AF217793; AAF33685.1; -.
DR   EMBL; AF217794; AAF33686.1; -.
DR   EMBL; AL121845; CAC03668.1; -.
DR   EMBL; BC017065; AAH17065.1; -.
DR   Genew; HGNC:11921; TNFRSF6B.
DR   MIM; 603361; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     29
FT   CHAIN       30    300       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 6B.
FT   REPEAT      31     70       TNFR-CYS 1.
FT   REPEAT      72    113       TNFR-CYS 2.
FT   REPEAT     115    150       TNFR-CYS 3.
FT   REPEAT     152    193       TNFR-CYS 4.
FT   DISULFID    49     62       BY SIMILARITY.
FT   DISULFID    52     70       BY SIMILARITY.
FT   DISULFID    73     88       BY SIMILARITY.
FT   DISULFID    91    105       BY SIMILARITY.
FT   DISULFID    95    113       BY SIMILARITY.
FT   DISULFID   115    126       BY SIMILARITY.
FT   DISULFID   132    150       BY SIMILARITY.
FT   DISULFID   153    168       BY SIMILARITY.
FT   DISULFID   174    193       BY SIMILARITY.
FT   CARBOHYD   173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   300 AA;  32679 MW;  F90AEE33718449AF CRC64;

  Query Match           100.0%;  Score 1634;  DB 1;  Length 300;
  Best Local Similarity  100.0%;  Pred. No. 6.7e-120;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
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RESULT 2
T11B_HUMAN
ID   T11B_HUMAN     STANDARD;      PRT;   401 AA.
AC   O00300; O60236; Q9UHP4;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 11B precursor
DE   (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN   TNFRSF11B OR OPG OR OCIF.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=97262071; PubMed=9108485;
RA   Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA   Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA   Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA   Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA   Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA   Suggs S., Boyle W.J.;
RT   "Osteoprotegerin: a novel secreted protein involved in the regulation
RT   of bone density.";
RL   Cell 89:309-319(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung cancer;
RX   MEDLINE=98151033; PubMed=9492069;
RA   Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
RA   Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
RA   Tsuda E., Morinaga T., Higashio K.;
RT   "Identity of osteoclastogenesis inhibitory factor (OCIF) and
RT   osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
RT   osteoclastogenesis in vitro.";
RL   Endocrinology 139:1329-1337(1998).
RN   [3]
RP   SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC   TISSUE=Placenta;
RX   MEDLINE=98351569; PubMed=9688283;
RA   Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
RT   "Cloning and characterization of the gene encoding human
RT   osteoprotegerin/osteoclastogenesis-inhibitory factor.";
RL   Eur. J. Biochem. 254:685-691(1998).
RN   [4]
RP   SEQUENCE FROM N.A., AND VARIANT ASN-3.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 22-36 AND 378-401.
RX   MEDLINE=98238645; PubMed=9571159;
RA   Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
RA   Morinaga T., Tsuda E., Higashio K.;
RT   "Characterization of monomeric and homodimeric forms of
RT   osteoclastogenesis inhibitory factor.";
RL   Biochem. Biophys. Res. Commun. 245:382-387(1998).
RN   [6]
RP   SEQUENCE OF 22-393 FROM N.A.
RC   TISSUE=Placenta;
RA   He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT   "Cloning and expression of osteoprotegerin from Homo sapiens.";
RL   Acta Biochim. Biophys. Sin. 31:680-684(1999).
RN   [7]
RP   SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
RX   MEDLINE=97312536; PubMed=9168977;
RA   Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
RA   Morinaga T., Higashio K.;
RT   "Isolation of a novel cytokine from human fibroblasts that
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RT   specifically inhibits osteoclastogenesis.";
RL   Biochem. Biophys. Res. Commun. 234:137-142(1997).
RN   [8]
RP   TRAIL BINDING.
RX   MEDLINE=98269100; PubMed=9603945;
RA   Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
RA   Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dodds R.A.,
RA   James I.E., Rosenberg M., Lee J.C., Young P.R.;
RT   "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
RL   J. Biol. Chem. 273:14363-14367(1998).
RN   [9]
RP   CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
RX   MEDLINE=98148058; PubMed=9478964;
RA   Yamaguchi K., Kinosaki M., Goto M., Kobayashi F., Tsuda E.,
RA   Morinaga T., Higashio K.;
RT   "Characterization of structural domains of human osteoclastogenesis
RT   inhibitory factor.";
RL   J. Biol. Chem. 273:5117-5123(1998).
RN   [10]
RP   REVIEW.
RX   MEDLINE=21395914; PubMed=11505389;
RA   Hofbauer L.C., Neubauer A., Heufelder A.E.;
RT   "Receptor activator of nuclear factor-kappaB ligand and
RT   osteoprotegerin: potential implications for the pathogenesis and
RT   treatment of malignant bone diseases.";
RL   Cancer 92:460-470(2001).
CC   -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC       its function in osteoclastogenesis. Inhibits the activation of
CC       osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC       homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC       play a role in preventing arterial calcification. May act as decoy
CC       receptor for TRAIL and protect against apoptosis. TRAIL binding
CC       blocks the inhibition of osteoclastogenesis.
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
CC       liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
CC       lymph node, trachea, adrenal gland, testis, and bone marrow.
CC       Detected at very low levels in brain, placenta and skeletal
CC       muscle. Highly expressed in fetal kidney, liver and lung.
CC   -!- INDUCTION: Upregulated by increasing calcium-concentration in the
CC       medium and estrogens. Downregulated by glucocorticoids.
CC   -!- PTM: N-glycosylated. Contains sialic acid residues.
CC   -!- PTM: N-terminus may be blocked.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U94332; AAB53709.1; -.
DR   EMBL; AB002146; BAA25910.1; -.
DR   EMBL; AB008822; BAA32076.1; -.
DR   EMBL; AB008821; BAA32076.1; JOINED.
DR   EMBL; BC030155; AAH30155.1; -.
DR   EMBL; AF134187; AAF20168.1; -.
DR   HSSP; P25942; 1CDF.
DR   Genew; HGNC:11909; TNFRSF11B.
DR   MIM; 602643; -.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
FT   SIGNAL       1     21
FT   CHAIN       22    401       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 11B.
FT   REPEAT      24     62       TNFR-CYS 1.
FT   REPEAT      65    105       TNFR-CYS 2.
FT   REPEAT     107    142       TNFR-CYS 3.
FT   REPEAT     145    185       TNFR-CYS 4.
FT   DOMAIN     198    269       DEATH 1.
FT   DOMAIN     270    365       DEATH 2.
FT   SITE       400    400       INVOLVED IN DIMERIZATION.
FT   DISULFID    41     54       BY SIMILARITY.
FT   DISULFID    44     62       BY SIMILARITY.
FT   DISULFID    65     80       BY SIMILARITY.
FT   DISULFID    83     97       BY SIMILARITY.
FT   DISULFID    87    105       BY SIMILARITY.
FT   DISULFID   107    118       BY SIMILARITY.
FT   DISULFID   124    142       BY SIMILARITY.
FT   DISULFID   145    160       BY SIMILARITY.
FT   DISULFID   166    185       BY SIMILARITY.
FT   CARBOHYD    98     98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   152    152       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   165    165       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   178    178       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      3      3       K -> N.
FT                                /FTId=VAR_013439.
FT   MUTAGEN    400    400       C->S: ABOLISHES DIMERIZATION.
FT   MUTAGEN    400    401       MISSING: ABOLISHES DIMERIZATION.
FT   CONFLICT   263    263       D -> A (IN REF. 1).
SQ   SEQUENCE   401 AA;  46040 MW;  EDF448B67D86C71E CRC64;

  Query Match             27.2%;  Score 444;  DB 1;  Length 401;
  Best Local Similarity   39.6%;  Pred. No. 1.7e-27;
  Matches   84;  Conservative   32;  Mismatches   86;  Indels   10;  Gaps    4;

Qy         11 LLCLVLALPALLPVPAVRGVAET--PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPT 68
              |||  |     | :        ||  | |   | ||  :|:| :|||||::: |     |
Db          4 LLCCAL---VFLDISIKWTTQETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKT 60

Qy         69 TCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLE 128
                | |||  :||  |:  : | ||: :| | :   : |: |||| | |: | :    |||:
Db         61 VCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLK 120

Qy        129 HASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSS 188
              | ||||| ||:  ||| :|| |: || | ||  :||   |: | ||:  || |   |:::
Db        121 HRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNAT 180

Qy        189 HDTLCTSCTGFPLSTRVPGAEE--CERAVIDF 218
              || :   |:|   ||:  | :   || |   |
Db        181 HDNI---CSGNSESTQKCGIDVTLCEEAFFRF 209


RESULT 3
T11B_RAT
ID   T11B_RAT       STANDARD;      PRT;   401 AA.
AC   O08727;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 11B precursor
DE   (Osteoprotegerin).
GN   TNFRSF11B OR OPG.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryonic intestine;
RX   MEDLINE=97262071; PubMed=9108485;
RA   Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA   Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
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RA   Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA   Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA   Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA   Suggs S., Boyle W.J.;
RT   "Osteoprotegerin: a novel secreted protein involved in the regulation
RT   of bone density.";
RL   Cell 89:309-319(1997).
CC   -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC       its function in osteoclastogenesis. Inhibits the activation of
CC       osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
CC       seems to depend on the local RANKL/OPG ratio. May also play a role
CC       in preventing arterial calcification. May act as decoy receptor
CC       for TRAIL and protect against apoptosis. TRAIL binding blocks the
CC       inhibition of osteoclastogenesis (By similarity).
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- INDUCTION: Upregulated by osteopontin.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U94330; AAB53707.1; -.
DR   HSSP; P25942; 1CDF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     21       BY SIMILARITY.
FT   CHAIN       22    401       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 11B.
FT   REPEAT      24     62       TNFR-CYS 1.
FT   REPEAT      65    105       TNFR-CYS 2.
FT   REPEAT     107    142       TNFR-CYS 3.
FT   REPEAT     145    185       TNFR-CYS 4.
FT   DOMAIN     198    269       DEATH 1.
FT   DOMAIN     270    365       DEATH 2.
FT   SITE       400    400       INVOLVED IN DIMERIZATION (BY SIMILARITY).
FT   DISULFID    41     54       BY SIMILARITY.
FT   DISULFID    44     62       BY SIMILARITY.
FT   DISULFID    65     80       BY SIMILARITY.
FT   DISULFID    83     97       BY SIMILARITY.
FT   DISULFID    87    105       BY SIMILARITY.
FT   DISULFID   107    118       BY SIMILARITY.
FT   DISULFID   124    142       BY SIMILARITY.
FT   DISULFID   145    160       BY SIMILARITY.
FT   DISULFID   166    185       BY SIMILARITY.
FT   CARBOHYD    98     98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   165    165       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   178    178       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   401 AA;  46192 MW;  FEC6A31F1D4E573A CRC64;

  Query Match           26.0%;  Score 425.5;  DB 1;  Length 401;
  Best Local Similarity   39.5%;  Pred. No. 4.6e-26;
  Matches   81;  Conservative   33;  Mismatches   86;  Indels    5;  Gaps    2;

Qy         34 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 93
              | |   | ||| :|:| :| |||:::: |     | | |||   ||  |:  : | ||:
Db         26 PKYLHYDPETGRQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDYSYTDSWHTSDECVYCSP 85

Qy         94 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 153
              :| | :   : |: |||| | |  | :    |||:| ||||| ||:  ||| :|| |: |
Db         86 VCKELQTVKQECNRTHNRVCECEEGRYLELEFCLKHRSCPPGLGVLQAGTPERNTVCKRC 145

Qy        154 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 211
              | | ||  :||   |: | ||::|||  |   |:::|| :   |:|   :|:  | :   |
Db        146 PDGFFSGETSSKAPCRKHTNCSSLGLLLIQKGNATHDNV---CSGNREATQNCGIDVTLC 202

Qy        212 ERAVIDFVAFQDISIKRLQRLLQAL 236
              | |   |     |    |  |: :|
Db        203 EEAFFRFAVPTKIIPNWLSVLVDSL 227


RESULT 4
T11B_MOUSE
ID   T11B_MOUSE     STANDARD;      PRT;   401 AA.
AC   O08712; O70202;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 11B precursor
DE   (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
GN   TNFRSF11B OR OPG OR OCIF.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Kidney;
RX   MEDLINE=97262071; PubMed=9108485;
RA   Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA   Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA   Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA   Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA   Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA   Suggs S., Boyle W.J.;
RT   "Osteoprotegerin: a novel secreted protein involved in the regulation
RT   of bone density.";
RL   Cell 89:309-319(1997).
RN   [2]
RP   SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
RP   AND ARG-296.
RC   STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
RX   MEDLINE=98382527; PubMed=9714833;
RA   Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
RA   Higashio K.;
RT   "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
RT   gene and its expression in embryogenesis.";
RL   Gene 215:339-343(1998).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=21060987; PubMed=10952716;
RA   Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
RA   Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
RA   Simonet W.S.;
RT   "Osteoprotegerin reverses osteoporosis by inhibiting endosteal
RT   osteoclasts and prevents vascular calcification by blocking a process
RT   resembling osteoclastogenesis.";
RL   J. Exp. Med. 192:463-474(2000).
CC   -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC       its function in osteoclastogenesis. Inhibits the activation of
CC       osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC       homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC       play a role in preventing arterial calcification. May act as decoy
CC       receptor for TRAIL and protect against apoptosis. TRAIL binding
CC       blocks the inhibition of osteoclastogenesis.
CC   -!- SUBUNIT: Homodimer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,
CC       intestines and calvaria. Highly expressed in decidua and placenta,
CC       and in embryo.
CC   -!- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,
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CC       whereas expression decreases at day 11 and increases from day 15
CC       to 17. On day 15 found in developing bone primordia,
CC       brachiocephalic artery and ductus arteriosus, left main bronchus,
CC       abdominal aorta and midgut.
CC   -!- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by
CC       1,25-dihdroxyvitamin D3 and parathyroid hormone.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 2 DEATH DOMAINS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U94331; AAB53708.1; -.
DR   EMBL; AB013898; BAA28269.1; -.
DR   EMBL; AB013903; BAA33388.1; -.
DR   EMBL; AB013899; BAA33388.1; JOINED.
DR   EMBL; AB013900; BAA33388.1; JOINED.
DR   EMBL; AB013901; BAA33388.1; JOINED.
DR   EMBL; AB013902; BAA33388.1; JOINED.
DR   HSSP; P25942; 1CDF.
DR   MGD; MGI:109587; Tnfrsf1lb.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   CHAIN        22    401       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 11B.
FT   REPEAT       24     62       TNFR-CYS 1.
FT   REPEAT       65    105       TNFR-CYS 2.
FT   REPEAT      107    142       TNFR-CYS 3.
FT   REPEAT      145    185       TNFR-CYS 4.
FT   DOMAIN      198    269       DEATH 1.
FT   DOMAIN      283    365       DEATH 2.
FT   SITE        400    400       INVOLVED IN DIMERIZATION (BY SIMILARITY).
FT   DISULFID     41     54       BY SIMILARITY.
FT   DISULFID     44     62       BY SIMILARITY.
FT   DISULFID     65     80       BY SIMILARITY.
FT   DISULFID     83     97       BY SIMILARITY.
FT   DISULFID     87    105       BY SIMILARITY.
FT   DISULFID    107    118       BY SIMILARITY.
FT   DISULFID    124    142       BY SIMILARITY.
FT   DISULFID    145    160       BY SIMILARITY.
FT   DISULFID    166    185       BY SIMILARITY.
FT   CARBOHYD     98     98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    165    165       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    178    178       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     138    138       R -> P (IN STRAINS 129/OLA AND NIH
FT                                 SWISS).
FT   VARIANT     161    161       I -> R (IN STRAINS 129/OLA AND NIH
FT                                 SWISS).
FT   VARIANT     165    165       N -> D (IN STRAINS 129/OLA AND NIH
FT                                 SWISS).
FT   VARIANT     288    288       S -> A (IN STRAINS 129/OLA AND NIH
FT                                 SWISS).
FT   VARIANT     296    296       L -> R (IN STRAINS 129/OLA AND NIH
FT                                 SWISS).
SQ   SEQUENCE   401 AA;  45923 MW;  CAA6102D3B312470 CRC64;

  Query Match             26.0%;  Score 424.5;  DB 1;  Length 401;
  Best Local Similarity   39.0%;  Pred. No. 5.5e-26;

  Matches   80;  Conservative   32;  Mismatches   88;  Indels    5;  Gaps    2;

Qy         34 PTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNV 93
              | |   | ||| :|:| :| |||:::: |     | | |||   || |:  : | ||:
Db         26 PKYLHYDPETGHQLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSP 85

Qy         94 LCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 153
              :| | :   : |: |||| | |  | :    |||:| |||||:||:  ||| :|| |: |
Db         86 VCKELQSVKQECNRTHNRVCECEEGRYLEIEFCLKHRSCPPGSGVVQAGTPERNTVCKKC 145

Qy        154 PPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEE--C 211
              | | ||  :||   |  | ||:  || |   |:::|| :   |:|   :|:  | :   |
Db        146 PDGFFSGETSSKAPCIKHTNCSTFGLLLIQKGNATHDNV---CSGNREATQKCGIDVTLC 202

Qy        212 ERAVIDFVAFQDISIKRLQRLLQAL 236
              | |   |     |    |  |: :|
Db        203 EEAFFRFAVPTKIIPNWLSVLVDSL 227


RESULT 5
TR1B_HUMAN
ID   TR1B_HUMAN     STANDARD;      PRT;   461 AA.
AC   P20333; Q16042;
DT   01-FEB-1991 (Rel. 17, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE   necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Etanercept)
DE   [Contains: Tumor necrosis factor binding protein 2 (TBPII)].
GN   TNFRSF1B OR TNFR2 OR TNFBR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90260639; PubMed=2160731;
RA   Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA   Dower S.K., Cosman D., Goodwin R.G.;
RT   "A receptor for tumor necrosis factor defines an unusual family of
RT   cellular and viral proteins.";
RL   Science 248:1019-1023(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91045991; PubMed=2172983;
RA   Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA   Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT   "A second tumor necrosis factor receptor gene product can shed a
RT   naturally occurring tumor necrosis factor inhibitor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96299745; PubMed=8661109;
RA   Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA   Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA   Brodeur G.M.;
RT   "Physical mapping and genomic structure of the human TNFR2 gene.";
RL   Genomics 35:94-100(1996).
RN   [4]
RP   SEQUENCE OF 37-461 FROM N.A.
RX   MEDLINE=91370690; PubMed=1966549;
RA   Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
RA   Brockhaus M., Lesslauer W.;
RT   "Two human TNF receptors have similar extracellular, but distinct
RT   intracellular, domain sequences.";
RL   Cytokine 2:231-237(1990).
RN   [5]
RP   SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=90349572; PubMed=2166946;
RA   Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA   Ringold G.M.;
RT   "Complementary DNA cloning of a receptor for tumor necrosis factor
RT   and demonstration of a shed form of the receptor.";
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RL   Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN   [6]
RP   SEQUENCE OF 27-31.
RX   MEDLINE=90110215; PubMed=2153136;
RA   Engelmann H., Novick D., Wallach D.;
RT   "Two tumor necrosis factor-binding proteins purified from human
RT   urine. Evidence for immunological cross-reactivity with cell surface
RT   tumor necrosis factor receptors.";
RL   J. Biol. Chem. 265:1531-1536(1990).
RN   [7]
RP   SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
RX   MEDLINE=91056048; PubMed=2173696;
RA   Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA   Brockhaus M.;
RT   "Purification and partial amino acid sequence analysis of two
RT   distinct tumor necrosis factor receptors from HL60 cells.";
RL   J. Biol. Chem. 265:20131-20138(1990).
RN   [8]
RP   CHARACTERIZATION.
RX   MEDLINE=93016040; PubMed=1328224;
RA   Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA   Lipari M.T., Goeddel D.V.;
RT   "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT   Characterization of ligand binding, internalization, and receptor
RT   phosphorylation.";
RL   J. Biol. Chem. 267:21172-21178(1992).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
RP   TRAF2.
RX   MEDLINE=99221490; PubMed=10206649;
RA   Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT   "Structural basis for self-association and receptor recognition of
RT   human TRAF2.";
RL   Nature 398:533-538(1999).
CC   -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
CC       approximately 5-fold lower affinity for homotrimeric
CC       TNFSF1/lymphotoxin-alpha.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
CC   -!- PTM: Phosphorylated; mainly on serine residues and with a very low
CC       level on threonine residues.
CC   -!- PTM: A soluble form (tumor necrosis factor binding protein 2) is
CC       produced from the membrane form by proteolytic processing.
CC   -!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and
CC       Wyeth-Ayerst). Used to treat moderate to servere rheumatoid
CC       arthritis (RA). Enbrel consist of the extracellular ligand-binding
CC       portion of TNFR2 linked to an Immuglobulin Fc chain. It binds to
CC       TNF-alpha and blocks its interactions with receptors.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
CC   -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
CC       WWW="http://www.enbrelinfo.com/".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M32315; AAA59929.1; -.
DR   EMBL; U52165; AAC50622.1; -.
DR   EMBL; U52156; AAC50622.1; JOINED.
DR   EMBL; U52157; AAC50622.1; JOINED.
DR   EMBL; U52158; AAC50622.1; JOINED.
DR   EMBL; U52159; AAC50622.1; JOINED.
DR   EMBL; U52160; AAC50622.1; JOINED.
DR   EMBL; U52161; AAC50622.1; JOINED.
DR   EMBL; U52162; AAC50622.1; JOINED.
DR   EMBL; U52163; AAC50622.1; JOINED.
DR   EMBL; U52164; AAC50622.1; JOINED.
DR   EMBL; M55994; AAA36755.1; -.
DR   EMBL; S63368; AAB19824.2; -.
DR   EMBL; M35857; AAA63262.1; -.
DR   PIR; A35356; A35356.
DR   PIR; A36007; A36007.
DR   PIR; A36475; A36475.
DR   PIR; B35010; B35010.
DR   PIR; A23666; A23666.
DR   PDB; 1CA9; 12-APR-99.
DR   Genew; HGNC:11917; TNFRSF1B.
DR   MIM; 191191; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
KW   Phosphorylation; Pharmaceutical; 3D-structure.
FT   SIGNAL       1     22
FT   CHAIN       23    461       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 1B, MEMBRANE FORM.
FT   CHAIN       27      ?       TUMOR NECROSIS FACTOR BINDING PROTEIN 2.
FT   DOMAIN      23    257       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   258    287       POTENTIAL.
FT   DOMAIN     288    461       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      39     76       TNFR-CYS 1.
FT   REPEAT      77    118       TNFR-CYS 2.
FT   REPEAT     119    162       TNFR-CYS 3.
FT   REPEAT     163    201       TNFR-CYS 4.
FT   DISULFID    40     53       BY SIMILARITY.
FT   DISULFID    54     67       BY SIMILARITY.
FT   DISULFID    57     75       BY SIMILARITY.
FT   DISULFID    78     93       BY SIMILARITY.
FT   DISULFID    96    110       BY SIMILARITY.
FT   DISULFID   100    118       BY SIMILARITY.
FT   DISULFID   120    126       BY SIMILARITY.
FT   DISULFID   134    143       BY SIMILARITY.
FT   DISULFID   137    161       BY SIMILARITY.
FT   DISULFID   164    179       BY SIMILARITY.
FT   CARBOHYD   171    171       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   193    193       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   141    141       R -> P (IN REF. 5).
FT   CONFLICT   196    196       M -> R (IN REF. 2 AND 5).
FT   CONFLICT   363    363       A -> T (IN REF. 5).
SQ   SEQUENCE   461 AA;  48291 MW;  603D0AE1CD69ACBF CRC64;

  Query Match           21.5%;  Score 351.5;  DB 1;  Length 461;
  Best Local Similarity   29.8%;  Pred. No. 2.9e-20;
  Matches   96;  Conservative   43;  Mismatches  122;  Indels   61;  Gaps   12;

Qy          8 GLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGE-----------RLVCAQCPPG 55
              || |     ||||        || ||  |   | |             :: |::| ||
Db         13 GLELWAAAHALPA--------QVAFTPYAP----EPGSTCRLREYYDQTAQMCCSKCSPG 60

Qy         56 TFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRC 115
                :  | : | | |  |    ||| ||::  |  |   |   : | :||    || | |
Db         61 QHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTC 120

Qy        116 RTGFFAHAG------FCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQ 169
              | |::           |     | || ||  ||| : :  |:|| ||||| ::||:: |:
Db        121 RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDICR 180

Qy        170 PHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRL 229
              ||: |  :     :||::| | :||| :  |  :  |||    : |  .     :
Db        181 PHQICNVVA----IPGNASMDAVCTSTS--PTRSMAPGAVHLPQPV-------STRSQHT 227

Qy        230 QRLLQALEAPE-----GWGPTPRA----GRAALQLKLRRRLTELLGAQDGALLVRLLQAL 280
              |   :   ||         ||:| |     |  || : |   :| |      | |:: ::  :
Db        228 QPTPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTAL-----GLLIIGVVNCV 282

Qy        281 --RVARMP-GLERSVRERFLP 298
                :| : |  |:|  :   ||
Db        283 IMTQVKKKPLCLQREAKVPHLP 304
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RESULT 6
TR1B_MOUSE
ID   TR1B_MOUSE     STANDARD;      PRT;   474 AA.
AC   P25119; P97893;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE   necrosis factor receptor 2) (TNF-R2) (p75).
GN   TNFRSF1B OR TNFR2 OR TNFR-2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91187885; PubMed=1849278;
RA   Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA   Wong G.H., Chen E.Y., Goeddel D.V.;
RT   "Cloning and expression of cDNAs for two distinct murine tumor
RT   necrosis factor receptors demonstrate one receptor is species
RT   specific.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91246168; PubMed=1645445;
RA   Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA   Copeland N.G., Jenkins N.A., Smith C.A.;
RT   "Molecular cloning and expression of the type 1 and type 2 murine
RT   receptors for tumor necrosis factor.";
RL   Mol. Cell. Biol. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE OF 1-26 FROM N.A.
RC   STRAIN=NOD;
RA   Jacob C.O., Liu J.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1-22 FROM N.A.
RC   TISSUE=Liver;
RA   Kissonerghis M., Fellowes R., Feldmann M., Chernajovsky Y.;
RL   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and
CC       approximately 5-fold lower affinity for homotrimeric
CC       TNFSF1/lymphotoxin-alpha (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M60469; AAA39752.1; -.
DR   EMBL; M59378; AAA40463.1; -.
DR   EMBL; U39488; AAA85021.1; -.
DR   EMBL; X87128; CAA60618.1; -.
DR   PIR; B38634; B38634.
DR   HSSP; P19438; 1NCF.
DR   MGD; MGI:1314883; Tnfrsf1b.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    474       TUMOR NECROSIS FACTOR RECEPTOR
FT                                 SUPERFAMILY MEMBER 1B.
FT   DOMAIN        23    258       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     259    288       POTENTIAL.
FT   DOMAIN       289    474       CYTOPLASMIC (POTENTIAL).
FT   REPEAT        39     77       TNFR-CYS 1.
FT   REPEAT        78    119       TNFR-CYS 2.
FT   REPEAT       120    164       TNFR-CYS 3.
FT   REPEAT       165    203       TNFR-CYS 4.
FT   DISULFID      40     54       BY SIMILARITY.
FT   DISULFID      55     68       BY SIMILARITY.
FT   DISULFID      58     76       BY SIMILARITY.
FT   DISULFID      79     94       BY SIMILARITY.
FT   DISULFID      97    111       BY SIMILARITY.
FT   DISULFID     101    119       BY SIMILARITY.
FT   DISULFID     121    127       BY SIMILARITY.
FT   DISULFID     136    145       BY SIMILARITY.
FT   DISULFID     139    163       BY SIMILARITY.
FT   DISULFID     166    181       BY SIMILARITY.
FT   CARBOHYD      69     69       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     195    195       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   474 AA;  50319 MW;  462EAE398C4D6563 CRC64;

  Query Match           20.3%;  Score 332.5;  DB 1;  Length 474;
  Best Local Similarity   29.7%;  Pred. No. 8.9e-19;
  Matches   81;  Conservative   44;  Mismatches  109;  Indels   39;  Gaps    9;

Qy         46 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC 105
              :: ||:|||| :|:  | : | | |  |    ||| ||    |  |:  |   : | |||
Db         52 QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRAC 111

Qy        106 HATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 158
              || | |  | :     |:|    |:  : | || || :   |: |  |: | |||| |
Db        112 TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF 171

Qy        159 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPGAEECERA 214
              | ::||:: |:||| |: |     :||::| | :|     : :  | :  |   |
Db        172 SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQ 227

Qy        215 VIDFVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLTELLGAQD 269
               :|    |:    :   :| :|      | ||      |  :| : |   :| |
Db        228 PLD----QEPGPSQTPSILTSL------GSTPIIEQSTKGGISLPIGLIVGVTSL----- 272

Qy        270 GALLVRLLQAL----RVARMPGLERSVRERFLP 298
              | |:: |:  :    |  :   |:|  :   :|
Db        273 GLLMLGLVNCIILVQRKKKPSCLQRDAKVPHVP 305


RESULT 7
TNR3_HUMAN
ID   TNR3_HUMAN     STANDARD;      PRT;   435 AA.
AC   P36941;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 3 precursor
DE   (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related
DE   protein) (Tumor necrosis factor C receptor).
GN   LTBR OR TNFRSF3 OR TNFCR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93252381; PubMed=8486360;
RA   Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT   "Construction and evaluation of a hncDNA library of human 12p
RT   transcribed sequences derived from a somatic cell hybrid.";
RL   Genomics 16:214-218(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
```

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RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   FUNCTION.
RX   MEDLINE=94225209; PubMed=8171323;
RA   Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA   Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT   "A lymphotoxin-beta-specific receptor.";
RL   Science 264:707-710(1994).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=99223511; PubMed=10207006;
RA   Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
RT   "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RT   death in HeLa cells.";
RL   J. Biol. Chem. 274:11868-11873(1999).
RN   [5]
RP   FUNCTION.
RX   MEDLINE=20261554; PubMed=10799510;
RA   Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA   Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT   "The lymphotoxin-beta receptor is necessary and sufficient for
RT   LIGHT-mediated apoptosis of tumor cells.";
RL   J. Biol. Chem. 275:14307-14315(2000).
CC   -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC       LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3
CC       and TRAF5. May play a role in the development of lymphoid organs.
CC   -!- SUBUNIT: Self-associates.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L04270; AAA36757.1; -.
DR   EMBL; BC026262; AAH26262.1; -.
DR   HSSP; P25942; 1CDF.
DR   Genew; HGNC:6718; LTBR.
DR   MIM; 600979; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     30       POTENTIAL.
FT   CHAIN       31    435       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 3.
FT   DOMAIN      31    227       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   228    248       POTENTIAL.
FT   DOMAIN     249    435       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      42     81       TNFR-CYS 1.
FT   REPEAT      82    124       TNFR-CYS 2.
FT   REPEAT     125    168       TNFR-CYS 3.
FT   REPEAT     169    211       TNFR-CYS 4.
FT   DISULFID    43     58       BY SIMILARITY.
FT   DISULFID    59     72       BY SIMILARITY.
FT   DISULFID    62     80       BY SIMILARITY.
FT   DISULFID    83     98       BY SIMILARITY.
FT   DISULFID   101    116       BY SIMILARITY.
FT   DISULFID   104    124       BY SIMILARITY.
FT   DISULFID   126    132       BY SIMILARITY.
FT   DISULFID   139    148       BY SIMILARITY.
FT   DISULFID   142    167       BY SIMILARITY.
FT   DISULFID   170    185       BY SIMILARITY.
FT   CARBOHYD    40     40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
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SQ   SEQUENCE   435 AA;  46709 MW;  624626E6022F656F CRC64;

  Query Match             19.3%;  Score 315;  DB 1;  Length 435;
  Best Local Similarity   31.8%;  Pred. No. 1.8e-17;
  Matches   89;  Conservative   29;  Mismatches  120;  Indels  42;  Gaps   12;

Qy          3 ALEGPGLSLLCLVLALPALLPVPAVRGVAETPTY-----PWRDA-----ETGERLVCAQC 52
              |   |||:   ||| |  ||      : |   | |        ||       |   |: |::|
Db          6 ATSAPGLAWGPLVLGLFGLLAASQPQAV---PPYASENQTCRDQEKEYYEPQHRICCSRC 62

Qy         53 PPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYL---ERCRYCNVLCGEREEEARACHATH 109
              ||||:|   | |   | |  |    | : ||||   : || |: : |   ||   | :
Db         63 PPGTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMG--LEEIAPCTSKR 120

Qy        110 NRACRCRTGFFAHAGFCLE--H----ASCPPGA-GVIAPGTPSQNTQCQPCPPGTFSASS 162
                ||: | |  | : ||  |    : ||||    :       | | ||  | |  :|
Db        121 KTQCRCQPGMFC-AAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHFQNTS 179

Qy        163 SSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQ 222
              | | :|||  |   ||    ||::  || | :    ||   : |       ::    |
Db        180 SPSARCQPHTRCENQGLVEAAPGTAQSDTTCKNPLE-PLPPEMSGTMLMLAVLLPLAFFL 238

Qy        223 DIS------------IKRLQRLLQALEAPEGWGPTPRAG 249
                ::             ::|  ||:    |:| || | ||
Db        239 LLATVFSCIWKSHPSLCRKLGSLLK--RRPQGEGPNPVAG 276
```

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RESULT 8
TR21_MOUSE
ID   TR21_MOUSE     STANDARD;      PRT;   655 AA.
AC   Q9EPU5; Q91XH9; Q91W77;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-
DE   related death receptor-6) (Death receptor 6).
GN   TNFRSF21 OR DR6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Kidney;
RA   Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RA   Minami M.;
RT   "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
RT   (DR6).";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Kidney;
RA   Kim V., Machleidt T., Shi W.-X., Wang X., Cai Z.;
RT   "Murine DR6: murine TNFR-related death receptor-6.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   FUNCTION.
RX   MEDLINE=21571606; PubMed=11714751;
RA   Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
RT   "Impaired c-Jun amino terminal kinase activity and T cell
RT   differentiation in death receptor 6-deficient mice.";
RL   J. Exp. Med. 194:1441-1448(2001).
CC   -!- FUNCTION: May activate NF-kappa-B and promote apoptosis (By
CC       similarity). May activate JNK and be involved in T-cell
CC       differentiation.
CC   -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC       May be involved in T-cell differentiation.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
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CC   -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in adult spleen,
CC       thymus, testis, prostate, ovary, small intestine, colon, brain,
CC       lung and kidney, and in fetal brain, liver and lung. Detected at
CC       lower levels in adult peripheral blood leukocytes, lung, and in
CC       fetal muscle, heart, kidney, small intestine and skin. Detected in
CC       T-cells, B-cells and monocytes. In T-cells expression is highest
CC       in Th0 cells, intermediate in Th2 cells and lower in Th1 cells.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF322069; AAG38115.1; -.
DR   EMBL; AY043489; AAK74193.1; -.
DR   EMBL; BC016420; AAH16420.1; -.
DR   HSSP; O14763; 1D0G.
DR   MGD; MGI:2151075; Tnfrsf21.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     41       POTENTIAL.
FT   CHAIN       42    655       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 21.
FT   DOMAIN      42    349       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   350    370       POTENTIAL.
FT   DOMAIN     371    655       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     415    498       DEATH.
FT   REPEAT      50     88       TNFR-CYS 1.
FT   REPEAT      90    131       TNFR-CYS 2.
FT   REPEAT     133    167       TNFR-CYS 3.
FT   REPEAT     170    211       TNFR-CYS 4.
FT   DISULFID    67     80       BY SIMILARITY.
FT   DISULFID    70     88       BY SIMILARITY.
FT   DISULFID    91    106       BY SIMILARITY.
FT   DISULFID   109    123       BY SIMILARITY.
FT   DISULFID   113    131       BY SIMILARITY.
FT   DISULFID   133    144       BY SIMILARITY.
FT   DISULFID   150    168       BY SIMILARITY.
FT   DISULFID   171    186       BY SIMILARITY.
FT   DISULFID   192    211       BY SIMILARITY.
FT   CARBOHYD    82     82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   252    252       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   257    257       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   278    278       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   352    352       W -> L (IN REF. 1).
FT   CONFLICT   523    523       M -> I (IN REF. 3).
SQ   SEQUENCE   655 AA;  71982 MW;  5EC7C51C7C99EFF7 CRC64;

  Query Match             17.8%;  Score 291.5;  DB 1;  Length 655;
  Best Local Similarity   28.6%;  Pred. No. 1.9e-15;
  Matches   73;  Conservative   37;  Mismatches  130;  Indels   15;  Gaps    3;

Qy         12 LCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCG 71
              | |:  |   :   |  : ::   ||   |  ||: | | :|| ||:|   |  |   |
Db         30 LLLLGFLSTITAQPEQKTLSLPGTYRHVDRTTGQVLTCDKCPAGTYVSEHCTNMSLRVCS 89

Qy         72 PCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHAS 131
                 ||   :|:  | :|||  |:  |     |   | |  :| | |  | :   | |  |
Db         90 SCPAGTFTRHENGIERCHDCSQPCPWPMIERLPCAALTDRECICPPGMYQSNGTCAPHTV 149

Qy        132 CPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDT 191
              || | ||   || ::: :|: |  ||||   ||  :|: | :|    | :  ||:   |
Db        150 CPVGWGVRKKGTENEDVRCKQCARGTFSDVPSSVMKCKAHTDCLGQNLEVVKPGTKETDN 209

Qy        192 LCTSCTGFPL---STRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRA 248
              :|    |  |   ||  | :     :  : :   |:     :         |:|   |
Db        210 VC----GMRLFFSSTNPPSSGTVTFSHPEHMESHDVPSSTYE--------PQGMNSTDSN 257

Qy        249 GRAALQLKLRRRLTE 263
                |::: |:   : |
Db        258 STASVRTKVPSGIEE 272


RESULT 9
TR21_HUMAN
ID   TR21_HUMAN     STANDARD;      PRT;   655 AA.
AC   O75509; Q96D86;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 21 precursor (TNFR-
DE   related death receptor-6) (Death receptor 6).
GN   TNFRSF21 OR DR6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98378343; PubMed=9714541;
RA   Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Yu G., Vincenz C.,
RA   Aggarwal B.B., Ni J., Dixit V.M.;
RT   "Identification and functional characterization of DR6, a novel death
RT   domain-containing TNF receptor.";
RL   FEBS Lett. 431:351-356(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Parker A.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, and Colon;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC   -!- SUBUNIT: Associates with TRADD.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -!- TISSUE SPECIFICITY: Highly expressed in heart, brain, placenta,
CC       pancreas, lymph node, thymus and prostate. Detected at lower
CC       levels in lung, skeletal muscle, kidney, testis, uterus, small
CC       intestine, colon, spleen, bone marrow and fetal liver. Very low
CC       levels were found in adult liver and peripheral blood leukocytes.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF068868; AAC34583.1; -.
DR   EMBL; AL096801; CAB75692.1; -.
DR   EMBL; BC017730; AAH17730.1; -.
DR   EMBL; BC010241; AAH10241.1; ALT_INIT.
DR   Genew; HGNC:13469; TNFRSF21.
DR   MIM; 605732; -.
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DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     41       POTENTIAL.
FT   CHAIN       42    655       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 21.
FT   DOMAIN      42    349       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   350    370       POTENTIAL.
FT   DOMAIN     371    655       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     415    498       DEATH.
FT   REPEAT      50     88       TNFR-CYS 1.
FT   REPEAT      90    131       TNFR-CYS 2.
FT   REPEAT     133    167       TNFR-CYS 3.
FT   REPEAT     170    211       TNFR-CYS 4.
FT   DISULFID    67     80       BY SIMILARITY.
FT   DISULFID    70     88       BY SIMILARITY.
FT   DISULFID    91    106       BY SIMILARITY.
FT   DISULFID   109    123       BY SIMILARITY.
FT   DISULFID   113    131       BY SIMILARITY.
FT   DISULFID   133    144       BY SIMILARITY.
FT   DISULFID   150    168       BY SIMILARITY.
FT   DISULFID   171    186       BY SIMILARITY.
FT   DISULFID   192    211       BY SIMILARITY.
FT   CARBOHYD    82     82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   141    141       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   252    252       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   257    257       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   278    278       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   289    289       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   655 AA;  71844 MW;  48939391C4852A33 CRC64;

  Query Match             17.6%;  Score 287;  DB 1;  Length 655;
  Best Local Similarity   34.3%;  Pred. No. 4.2e-15;
  Matches   58;  Conservative   23;  Mismatches   88;  Indels    0;  Gaps    0;

Qy         35 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVL 94
              ||    |  ||: | | :|| ||:|    |    |    |  ||    :|:  | :|:|  |: .
Db         53 TYRHVDRATGQVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQP 112

Qy         95 CGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCP 154
                 |     |  | |  :| | |  | |      |  |  || | ||   || ::: :|: |
Db        113 CPWPMIEKLPCAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRKKGTETEDVRCKQCA 172

Qy        155 PGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLST 203
                ||||   ||  :|: : :| :  | :  ||:   | :| :   |  ||
Db        173 RGTFSDVPSSVMKCKAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSST 221


RESULT 10
TNR3_MOUSE
ID   TNR3_MOUSE     STANDARD;      PRT;   415 AA.
AC   P50284;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 3 precursor
DE   (Lymphotoxin-beta receptor).
GN   LTBR OR TNFRSF3 OR TNFCR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CVB; TISSUE=Lung;
RX   MEDLINE=96072804; PubMed=7594541;
RA   Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA   Browning J.L., Ware C.F.;
RT   "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT   and expression.";
RL   J. Immunol. 155:5280-5288(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96163885; PubMed=8586432;
RA   Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA   Honjo T.;
RT   "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT   sequence trap and chromosomal mapping.";
RL   Genomics 30:312-319(1995).
CC   -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC       LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3
CC       and TRAF5. May play a role in the development of lymphoid organs
CC       (By similarity).
CC   -!- SUBUNIT: Self-associates (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U29173; AAA68964.1; -.
DR   EMBL; L38423; AAB00846.1; -.
DR   EMBL; U30798; AAA81334.1; -.
DR   HSSP; O14763; 1D0G.
DR   MGD; MGI:104875; Ltbr.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     30       POTENTIAL.
FT   CHAIN       31    415       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 3.
FT   DOMAIN      31    223       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   224    244       POTENTIAL.
FT   DOMAIN     245    415       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      42     81       TNFR-CYS 1.
FT   REPEAT      82    124       TNFR-CYS 2.
FT   REPEAT     125    170       TNFR-CYS 3.
FT   REPEAT     171    213       TNFR-CYS 4.
FT   DISULFID    43     58       BY SIMILARITY.
FT   DISULFID    59     72       BY SIMILARITY.
FT   DISULFID    62     80       BY SIMILARITY.
FT   DISULFID    83     98       BY SIMILARITY.
FT   DISULFID   101    116       BY SIMILARITY.
FT   DISULFID   104    124       BY SIMILARITY.
FT   DISULFID   126    132       BY SIMILARITY.
FT   DISULFID   139    150       BY SIMILARITY.
FT   DISULFID   142    169       BY SIMILARITY.
FT   DISULFID   172    187       BY SIMILARITY.
FT   CARBOHYD    40     40       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   415 AA;  44956 MW;  29B326A566AEF661 CRC64;

  Query Match             17.0%;  Score 277;  DB 1;  Length 415;
  Best Local Similarity   31.2%;  Pred. No. 1.6e-14;
  Matches   88;  Conservative   29;  Mismatches  105;  Indels   60;  Gaps   14;

Qy          6 GP---GLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERL---VCAQCPPGTFVQ 59
              ||   ||| | || : | |:|   :    |  |   :| |  | :    |::|||| ||
```

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Db         15 GPLLLGLSGL-LVASQPQLVPPYRI----ENQTCWDQDKEYYEPMHDVCCSRCPPGEFVF 69

Qy         60 RPCRRDSPTTCGPCPPRHYTQFWNYL---ERCRYCNVLCGEREEEARACHATHNRACRCR 116
                | |   | |  ||   | : ||:|   : || |::: |   ||   | :     |||:
Db         70 AVCSRSQDTVCKTCPHNSYNEHWNHLSTCQLCRPCDIVLG--FEEVAPCTSDRKAECRCQ 127

Qy        117 TGFFAHAGFCL----EHASCPPGAGVIA-PGTPSQNT--------QCQPCPPGTFSASSS 163
               |       |:    |   |     |:  ||| :: |         | || || |  :||
Db        128 PGM-----SCVYLDNECVHCEEERLVLCQPGTEAEVTDEIMDTDVNCVPCKPGHFQNTSS 182

Qy        164 SSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAF-- 221
                :||||  |   ||    ||:|  ||:|        :   |||      ::  | |
Db        183 PRARCQPHTRCEIQGLVEAAPGTSYSDTICK-------NPPEPGAMLLLAILLSLVLFLL 235

Qy        222 -----------QDISIKRLQRLLQALEAPEGWG----PTPRA 248
                         ::|  ||:    |||       | |||
Db        236 FTTVLACAWMRHPSLCRKLGTLLK--RHPEGEESPPCPAPRA 275


RESULT 11
CRMB_VARV
ID   CRMB_VARV      STANDARD;      PRT;   349 AA.
AC   P34015; Q89098; Q85407; Q89118;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Soluble TNF receptor II precursor (cytokine response modifying protein
DE   B).
GN   CRMB OR G2R OR G4R.
OS   Variola virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10255;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=India-1967 / Isolate Ind3;
RX   MEDLINE=93202281; PubMed=8384129;
RA   Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT   "Genes of variola and vaccinia viruses necessary to overcome the host
RT   protective mechanisms.";
RL   FEBS Lett. 319:80-83(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bangladesh-1975;
RX   MEDLINE=94088747; PubMed=8264798;
RA   Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,
RA   Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
RA   Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
RA   Venter C.J.;
RT   "Potential virulence determinants in terminal regions of variola
RT   smallpox virus genome.";
RL   Nature 366:748-751(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Garcia-1966, and Somalia-1977;
RA   Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
RA   Totmenin A.V., Shchelkunov S.N., Esposito J.J.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Garcia-1966;
RX   MEDLINE=20107289; PubMed=10639322;
RA   Shchelkunov S.N., Totmenin A.V., Loparev V.N., Safronov P.F.,
RA   Gutorov V.V., Chizhikov V.E., Knight J.C., Parsons J.M., Massung R.F.,
RA   Esposito J.J.;
RT   "Alastrim smallpox variola minor virus genome DNA sequences.";
RL   Virology 266:361-386(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Butler-1952, Chimp 9-4, Garcia-1966, and Somalia-1977;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC       the modification of TNF-mediated antiviral processes (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X69198; CAA49137.1; -.
DR   EMBL; X67117; CAA47540.1; -.
DR   EMBL; L22579; AAA60933.1; -.
DR   EMBL; U18339; AAA69407.1; -.
DR   EMBL; U18341; AAA69467.1; -.
DR   EMBL; Y16780; CAB54798.1; -.
DR   EMBL; U88146; AAB94371.1; -.
DR   EMBL; U88148; AAB94373.1; -.
DR   EMBL; U88149; AAB94374.1; -.
DR   EMBL; U88152; AAB94377.1; -.
DR   PIR; D36858; D36858.
DR   PIR; S35987; S35987.
DR   PIR; S46888; S46888.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    349       SOLUBLE TNF RECEPTOR II.
FT   REPEAT       31     66       TNFR-CYS 1.
FT   REPEAT       67    108       TNFR-CYS 2.
FT   DISULFID     32     43       BY SIMILARITY.
FT   DISULFID     44     57       BY SIMILARITY.
FT   DISULFID     47     65       BY SIMILARITY.
FT   DISULFID     68     83       BY SIMILARITY.
FT   DISULFID     86    100       BY SIMILARITY.
FT   DISULFID     90    108       BY SIMILARITY.
FT   CARBOHYD    101    101       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    189    189       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    215    215       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    248    248       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      17     17       MISSING (IN STRAINS BANGLADESH-1975 AND
FT                                CHIMP 9-4).
FT   VARIANT     160    160       H -> Y (IN STRAINS BUTLER-1952, GARCIA-
FT                                1966 AND SOMALIA-1977).
FT   VARIANT     165    165       A -> T (IN STRAINS BUTLER-1952 AND
FT                                GARCIA-1966).
FT   VARIANT     182    182       E -> K (IN STRAIN SOMALIA-1977).
FT   VARIANT     274    274       A -> E (IN STRAIN SOMALIA-1977).
FT   VARIANT     335    335       N -> D (IN STRAINS BUTLER-1952 AND
FT                                GARCIA-1966).
FT   VARIANT     339    339       P -> L (IN STRAINS BUTLER-1952 AND
FT                                GARCIA-1966).
SQ   SEQUENCE   349 AA;  38189 MW;  D45D40B5C6E780EF CRC64;

  Query Match             16.1%;  Score 262.5;  DB 1;  Length 349;
  Best Local Similarity   30.0%;  Pred. No. 1.7e-13;
  Matches   62;  Conservative   29;  Mismatches  103;  Indels   13;  Gaps    3;

Qy          9 LSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPT 68
                | | |:::      |     |  :  |          | |  |||||:  | |   : |
Db         10 LFLSCIIINGRDAAPYTPPNGKCKDTEY------KRHNLCCLSCPPGTYASRLCDSKTNT 63
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Qy          69 TCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF------AH 122
               | ||    :|   |:|  |  ||  |   : | |:|: |||| | |  |::      :
Db          64 QCTPCGSGTFTSRNNHLPACLSCNGRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSG 123

Qy         123 AGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALN 182
                 |:    |  | || :  |   :  | ||  ||:| : ||:::|:|  | |   : :
Db         124 CKACVSQTKCGIGYGV-SGHTSVGDVICSPCGFGTYSHTVSSADKCEPVPNNTFNYIDVE 182

Qy         183 VPGSSSHDTLCTSCTGFPLSTRVPGAE 209
               :     :|| ||  |   ||  :  :|
Db         183 ITLYPVNDTSCTRTTTTGLSESILTSE 209


RESULT 12
CRMB_CAMPS
ID   CRMB_CAMPS     STANDARD;      PRT;   349 AA.
AC   Q8UYA7;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Soluble TNF receptor II precursor (cytokine response modifying protein
DE   B).
GN   (CRMB1 OR CMP2L OR CMLV002) AND (CRMB2 OR CMP205R OR CMLV210).
OS   Camelpox virus (strain CMS), and
OS   Camelpox virus (strain M-96).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=203172, 203173;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CMS;
RX   PubMed=11907336;
RA   Gubser C., Smith G.L.;
RT   "The sequence of camelpox virus shows it is most closely related to
RT   variola virus, the cause of smallpox.";
RL   J. Gen. Virol. 83:855-872(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=M-96;
RA   Afonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L.,
RA   Kerembekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;
RT   "The genome of camelpox virus.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC       the modification of TNF-mediated antiviral processes (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY009089; AAG37456.1; -.
DR   EMBL; AY009089; AAG37718.1; -.
DR   EMBL; AF438165; AAL73920.1; -.
DR   EMBL; AF438165; AAL73917.1; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     19       POTENTIAL.
FT   CHAIN       20    349       SOLUBLE TNF RECEPTOR II.
FT   REPEAT      31     65       TNFR-CYS 1.
FT   REPEAT      67    108       TNFR-CYS 2.
FT   DISULFID    32     43       BY SIMILARITY.
FT   DISULFID    44     57       BY SIMILARITY.
FT   DISULFID    47     65       BY SIMILARITY.
FT   DISULFID    68     83       BY SIMILARITY.
FT   DISULFID    86    100       BY SIMILARITY.
FT   DISULFID    90    108       BY SIMILARITY.
FT   CARBOHYD   101    101       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   189    189       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   248    248       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   349 AA;  38064 MW;  EA412AF991E087F3 CRC64;

  Query Match             16.0%;  Score 261.5;  DB 1;  Length 349;
  Best Local Similarity   29.0%;  Pred. No. 2.1e-13;
  Matches   60;  Conservative   33;  Mismatches  101;  Indels   13;  Gaps    3;

Qy           9 LSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPT 68
               | | |:::    : |     |  :   |         | |  |||||:  | |   : |
Db          10 LFLSCIIINGRDVTPYAPSNGKCKDNEY------KRHNLCCLSCPPGTYASRLCDSKTNT 63

Qy          69 TCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF------AH 122
               |. ||    :|   |:|  |  ||  |   : | |:|: |||| | |  |::      :
Db          64 QCTPCGSGTFTSRNNHLPACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCILKGSSG 123

Qy         123 AGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALN 182
                 |:    |  | || :  | : :  | ||  ||:| : ||:::|:|  : |   : :
Db         124 CKACVSQTKCGIGYGV-SGHTSAGDVICSPCGLGTYSRTVSSADKCEPVPSNTFNYIDVE 182

Qy         183 VPGSSSHDTLCTSCTGFPLSTRVPGAE 209
               :     :|| ||  |   :|  :  :|
Db         183 INLYPVNDTSCTRTTTTGISESISTSE 209


RESULT 13
CRMB_COWPX
ID   CRMB_COWPX     STANDARD;      PRT;   351 AA.
AC   O73559;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Soluble TNF receptor II precursor (cytokine response modifying protein
DE   B).
GN   (CRMB1 OR D2L) AND (CRMB2 OR H4R).
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10243;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GRI-90 / Grishak;
RX   MEDLINE=98229462; PubMed=9568042;
RA   Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
RA   Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT   "The genomic sequence analysis of the left and right species-specific
RT   terminal region of a cowpox virus strain reveals unique sequences and
RT   a cluster of intact ORFs for immunomodulatory and host range
RT   proteins.";
RL   Virology 243:432-460(1998).
RN   [2]
RP   FUNCTION.
RC   STRAIN=Brighton red;
RX   PubMed=8091665;
RA   Hu F.Q., Smith C.A., Pickup D.J.;
RT   "Cowpox virus contains two copies of an early gene encoding a soluble
RT   secreted form of the type II TNF receptor.";
RL   Virology 204:343-356(1994).
CC   -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC       the modification of TNF-mediated antiviral processes.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; Y11842; CAA72578.1; -.
DR   EMBL; Y15035; CAA75306.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    351       SOLUBLE TNF RECEPTOR II.
FT   REPEAT       31     67       TNFR-CYS 1.
FT   REPEAT       69    110       TNFR-CYS 2.
FT   DISULFID     32     43       BY SIMILARITY.
FT   DISULFID     44     57       BY SIMILARITY.
FT   DISULFID     47     67       BY SIMILARITY.
FT   DISULFID     70     85       BY SIMILARITY.
FT   DISULFID     88    102       BY SIMILARITY.
FT   DISULFID     92    110       BY SIMILARITY.
FT   CARBOHYD    103    103       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    191    191       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    250    250       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   351 AA;  38253 MW;  57CAE73EF4E5D7C7 CRC64;

  Query Match             15.8%;  Score 258.5;  DB 1;  Length 351;
  Best Local Similarity   29.2%;  Pred. No. 3.6e-13;
  Matches   61;  Conservative   34;  Mismatches   99;  Indels   15;  Gaps    4;

Qy          9 LSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPC--RRDS 66
              | | |:::    : |    .|  :   |          | |  |||||:  | |  : ::
Db         10 LFLSCIIINGRDIAPHAPSNGKCKDNEY------NRHNLCCLSCPPGTYASRLCDSKTNT 63

Qy         67 PTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF------ 120
               | | ||    :|   |:|  |  ||  |   : | |:|: |||| | |  |::
Db         64 NTQCTPCGSGTFTSRNNHLPACLSCNGRCDSNQVETRSCNTTHNRICECAPGYYCLLKGS 123

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
               :    |:    |  | || :  | : :  | ||  ||:| : ||:::|:|  : |   :
Db        124 SGCKACVSQTKCGIGYGV-SGHTSTGDVVCSPCGLGTYSHTVSSADKCEPVPSNTFNYID 182

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
               : :     :|| ||  |   ||  :  :|
Db        183 VEINLYPVNDTSCTRTTTGLSESISTSE 211


RESULT 14
TR14_HUMAN
ID   TR14_HUMAN     STANDARD;      PRT;   283 AA.
AC   Q92956; Q9UM65; Q96J31; Q8WXR1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 14 precursor
DE   (Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)
DE   (TR2).
GN   TNFRSF14 OR HVEM OR HVEA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cervical adenocarcinoma;
RX   MEDLINE=97053782; PubMed=8898196;
RA   Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
RT   "Herpes simplex virus-1 entry into cells mediated by a novel member of
RT   the TNF/NGF receptor family.";
RL   Cell 87:427-436(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97306336; PubMed=9162061;
RA   Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
RA   Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
RA   Porter T.G., Truneh A., Young P.R.;
RT   "A newly identified member of the tumor necrosis factor receptor
RT   superfamily with a wide tissue distribution and involvement in
RT   lymphocyte activation.";
RL   J. Biol. Chem. 272:14272-14276(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Zhang W., Wan T., Cao X.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND ILE-241.
RX   MEDLINE=21629477; PubMed=11756979;
RA   Struyf F., Posavad C.M., Keyaerts E., Van Ranst M., Corey L.,
RA   Spear P.G.;
RT   "Search for polymorphisms in the genes for herpesvirus entry mediator,
RT   Nectin-1, and Nectin-2 in immune seronegative individuals.";
RL   J. Infect. Dis. 185:36-44(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
RX   MEDLINE=21403268; PubMed=11511370;
RA   Carfi A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,
RA   Eisenberg R.J., Wiley D.C.;
RT   "Herpes simplex virus glycoprotein D bound to the human receptor
RT   HveA.";
RL   Mol. Cell 8:169-179(2001).
CC   -!- FUNCTION: Receptor for TNFSF14/LIGHT and homotrimeric
CC       TNFSF1/lymphotoxin-alpha. Involved in lymphocyte activation. Plays
CC       an important role in HSV pathogenesis because it enhanced the
CC       entry of several wildtype HSV strains of both serotypes into CHO
CC       cells, and mediated HSV entry into activated human T cells.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
CC       IN LUNG, SPLEEN, AND THYMUS.
CC   -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U70321; AAB58354.1; -.
DR   EMBL; U81232; AAD00505.1; -.
DR   EMBL; AF153978; AAF75588.1; -.
DR   EMBL; AF373877; AAL47717.1; -.
DR   EMBL; AF373878; AAL47718.1; -.
DR   EMBL; BC002794; AAH02794.1; -.
DR   PDB; 1JMA; 26-SEP-01.
DR   Genew; HGNC:11912; TNFRSF14.
DR   MIM; 602746; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
KW   3D-structure.
FT   SIGNAL        1     38       POTENTIAL.
FT   CHAIN        39    283       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 14.
FT   DOMAIN       39    202       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    203    223       POTENTIAL.
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FT   DOMAIN      224    283       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       42     75       TNFR-CYS 1.
FT   REPEAT       78    119       TNFR-CYS 2.
FT   REPEAT      121    162       TNFR-CYS 3.
FT   DISULFID     42     53
FT   DISULFID     54     67
FT   DISULFID     57     75
FT   DISULFID     78     93
FT   DISULFID     96    111
FT   DISULFID     99    119
FT   DISULFID    121    138
FT   DISULFID    127    135
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      17     17       K -> R.
FT                                /FTId=VAR_013007.
FT   VARIANT     241    241       V -> I.
FT                                /FTId=VAR_013440.
SQ   SEQUENCE   283 AA;  30392 MW;  46CE13C2C70242C1 CRC64;

  Query Match             15.1%;  Score 246;  DB 1;  Length 283;
  Best Local Similarity   35.4%;  Pred. No. 2.7e-12;
  Matches   69;  Conservative   16;  Mismatches   88;  Indels   22;  Gaps    8;

Qy          7 PGLSLLCLVLALPAL---LPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCR 63
              |   :| ||| |  |       ||:   |   ||      |    | :| ||  |:  |
Db         16 PKTDVLRLVLYLTFLGAPCYAPALPSCKE-DEYP-----VGSE-CCPKCSPGYRVKEACG 68

Qy         64 RDSPTTCGPCPPRHYTQFWNYLER---CRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
                : | | ||||  |    | | :   |: |:   | |   :| |  | |  | |  | |
Db         69 ELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCDPAMGLR--ASRNCSRTENAVCGCSPGHF 126

Qy        121 A------HAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNC 174
                   |   |  :|:  ||  |   || ||:| || |||||||  : : |:||    |
Db        127 CIVQDGDHCAACRAYATSSPGQRVQKGGTESQDTLCQNCPPGTFS-PNGTLEECQHQTKC 185

Qy        175 TALGLALNVPGSSSH 189
              : |     ||||
Db        186 SWLVTKAGAGTSSSH 200


RESULT 15
TR11_HUMAN
ID   TR11_HUMAN     STANDARD;      PRT;   616 AA.
AC   Q9Y6Q6;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 11A precursor
DE   (Receptor activator of NF-KB) (Osteoclast differentiation factor
DE   receptor) (ODFR).
GN   TNFRSF11A OR RANK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dendritic cell;
RX   MEDLINE=98032977; PubMed=9367155;
RA   Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA   Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA   Galibert L.;
RT   "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT   and dendritic-cell function.";
RL   Nature 390:175-179(1997).
RN   [2]
RP   FUNCTION.
RX   MEDLINE=99097247; PubMed=9878548;
RA   Nakagawa N., Kinosaki M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA   Morinaga T., Higashio K.;
RT   "RANK is the essential signaling receptor for osteoclast
RT   differentiation factor in osteoclastogenesis.";
RL   Biochem. Biophys. Res. Commun. 253:395-400(1998).
RN   [3]
RP   VARIANT FEO 16-L--L-21 DUPL, VARIANT PDB2 13-A--L-21 DUPL, AND VARIANT
RP   V-192.
RX   MEDLINE=20082806; PubMed=10615125;
RA   Hughes A.E., Ralston S.H., Marken J., Bell C., MacPherson H.,
RA   Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
RA   Anderson D.M.;
RT   "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
RT   familial expansile osteolysis.";
RL   Nat. Genet. 24:45-48(2000).
CC   -!- FUNCTION: Receptor for TNFSF11/RANKL/TRANCE/OPGL; essential for
CC       RANKL-mediated osteoclastogenesis. Involved in the regulation of
CC       interactions between T-cells and dendritic cells.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
CC       SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
CC       GLAND.
CC   -!- DISEASE: DEFECTS IN TNFRSF11A ARE THE CAUSE OF FAMILIAL EXPANSILE
CC       OSTEOLYSIS (FEO), A RARE AUTOSOMAL DOMINANT BONE DISORDER
CC       CHARACTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELLING. THE
CC       OSTEOLYTIC LESIONS DEVELOP USUALLY IN THE LONG BONES DURING EARLY
CC       ADULTHOOD. FEO IS OFTEN ASSOCIATED WITH EARLY ONSET DEAFNESS AND
CC       LOSS OF DENTITION.
CC   -!- DISEASE: DEFECTS IN TNFRSF11A ARE A CAUSE OF FAMILIAL PAGET
CC       DISEASE OF BONE, ALSO KNOWN AS PAGET DISEASE OF BONE 2 (PDB2). IT
CC       IS A BONE REMODELLING DISORDER WITH CLINICAL SIMILARITIES TO FEO.
CC       UNLIKE FEO, HOWEVER, AFFECTED INDIVIDUALS HAVE INVOLVEMENT OF THE
CC       AXIAL SKELETON WITH LESIONS IN THE SPINE, PELVIS AND SKULL.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF018253; AAB86809.1; -.
DR   HSSP; P25942; 1CDF.
DR   Genew; HGNC:11908; TNFRSF11A.
DR   MIM; 603499; -.
DR   MIM; 174810; -.
DR   MIM; 602080; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
KW   Disease mutation.
FT   SIGNAL        1     29       POTENTIAL.
FT   CHAIN        30    616       TUMOR NECROSIS FACTOR RECEPTOR
FT                                SUPERFAMILY MEMBER 11A.
FT   DOMAIN       30    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    213    233       POTENTIAL.
FT   DOMAIN      234    616       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       34     68       TNFR-CYS 1.
FT   REPEAT       71    112       TNFR-CYS 2.
FT   REPEAT      114    151       TNFR-CYS 3.
FT   REPEAT      154    194       TNFR-CYS 4.
FT   DISULFID     34     46       BY SIMILARITY.
FT   DISULFID     47     60       BY SIMILARITY.
FT   DISULFID     50     68       BY SIMILARITY.
FT   DISULFID     71     86       BY SIMILARITY.
FT   DISULFID     92    112       BY SIMILARITY.
FT   DISULFID    114    127       BY SIMILARITY.
FT   DISULFID    133    151       BY SIMILARITY.
FT   CARBOHYD    105    105       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    174    174       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      21     21       L -> LALLLLCALL (IN PDB2).
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FT                                /FTId=VAR_011516.
FT   VARIANT      21     21       L -> LLLCALL (IN FEO).
FT                                /FTId=VAR_011517.
FT   VARIANT     192    192       A -> V.
FT                                /FTId=VAR_011518.
SQ   SEQUENCE   616 AA;  66033 MW;  E3DE9A7A08196F81 CRC64;

  Query Match             14.6%;  Score 239;  DB 1;  Length 616;
  Best Local Similarity   30.1%;  Pred. No. 2.1e-11;
  Matches   63;  Conservative   29;  Mismatches   93;  Indels   24;  Gaps    7;

Qy          9 LSLLCLVLA-LPALLPVPAVRGVAETPTYPWRDAETGERL--VCAQCPPGTFVQRPCRRD 65
              | ||| :|| |   | :           |    :  | |   | :| || ::   |
Db         14 LLLLCALLARLQVALQIAP----------PCTSEKHYEHLGRCCNKCEPGKYMSSKCTTT 63

Qy         66 SPTTCGPCPPRHYTQFWNYLERC---RYCNVLCGEREEEARACHATHNRACRCRTGFF-- 120
              | : | || |  |   ||  ::|   : |:   |:      | ::|  | | |  |:
Db         64 SDSVCLPCGPDEYLDSWNEEDKCLLHKVCDT--GKALVAVVAGNSTTPRRCACTAGYHWS 121

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
                  |  :  | || |   |   :::| |:||  | || : ||:::|:|  ||| ||
Db        122 QDCECCRRNTECAPGLGAQHPLQLNKDTVCKPCLAGYFSDAFSSTDKCRPWTNCTFLGKR 181

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              :   |:   | :|:|     |  | |  |
Db        182 VEHHGTEKSDAVCSS----SLPARKPPNE 206


Search completed: July 16, 2003, 19:37:29
Job time : 24 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 16, 2003, 19:28:49 ; Search time 81 Seconds
(without alignments)
763.137 Million cell updates/sec

Title: US-09-935-727-2
Perfect score: 1634
Sequence: 1 MRALEGPGLSLLCLVLALPA.....RVARMPGLERSVRERFLPVH 300

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	500	30.6	285	13	Q90W71	Q90w71 oncorhynchu
2	487	29.8	285	13	Q90YS6	Q90ys6 oncorhynchu
3	395	24.2	302	13	Q9PUS0	Q9pus0 salvelinus
4	333.5	20.4	459	11	Q62327	Q62327 mus musculu
5	327	20.0	482	11	O88734	O88734 mus musculu
6	313.5	19.2	433	11	Q91ZM6	Q91zm6 rattus norv
7	293.5	18.0	651	13	Q98SM6	Q98sm6 gallus gall
8	282.5	17.3	348	12	O57277	O57277 monkeypox v
9	280.5	17.2	348	12	O57103	O57103 monkeypox v
10	280.5	17.2	348	12	O57108	O57108 monkeypox v
11	276	16.9	349	12	O57100	O57100 monkeypox v
12	274	16.8	349	12	O57101	O57101 monkeypox v
13	274	16.8	349	12	O57102	O57102 monkeypox v
14	274	16.8	349	12	O57291	O57291 monkeypox v
15	273	16.7	349	12	O57099	O57099 monkeypox v
16	265	16.2	350	12	O57116	O57116 cowpox viru
17	264.5	16.2	355	12	Q85308	Q85308 cowpox viru
18	262.5	16.1	349	12	O57110	O57110 variola vir
19	262.5	16.1	349	12	O57111	O57111 variola vir
20	262.5	16.1	349	12	Q89098	Q89098 variola vir
21	262.5	16.1	349	12	Q89118	Q89118 variola vir
22	262	16.0	348	12	O57112	O57112 variola vir
23	262	16.0	348	12	Q85407	Q85407 variola vir
24	261.5	16.0	349	12	O57098	O57098 camelpox vi
25	261.5	16.0	349	12	Q8UYA7	Q8uya7 camelpox vi
26	261.5	16.0	349	12	O57284	O57284 camelpox vi
27	259.5	15.9	349	12	O57305	O57305 cowpox viru
28	259.5	15.9	360	12	O57118	O57118 cowpox viru
29	258.5	15.8	351	12	O57117	O57117 cowpox viru
30	258.5	15.8	351	12	O73559	O73559 cowpox viru
31	257.5	15.8	326	12	O57120	O57120 cowpox viru
32	257.5	15.8	349	12	O57097	O57097 camelpox vi
33	254.5	15.6	326	12	O57122	O57122 cowpox viru
34	254.5	15.6	349	12	O57109	O57109 variola vir
35	253.5	15.5	347	12	O57115	O57115 cowpox viru
36	251.5	15.4	347	12	O57119	O57119 cowpox viru
37	250.5	15.3	351	12	O57121	O57121 cowpox viru
38	249	15.2	283	6	Q9XSZ8	Q9xsz8 cercopithec
39	245.5	15.0	350	12	O57123	O57123 cowpox viru
40	232	14.2	278	6	Q8SQ34	Q8sq34 sus scrofa
41	230.5	14.1	276	13	Q9DDD2	Q9ddd2 gallus gall
42	228.5	14.0	277	6	Q8WMQ2	Q8wmq2 ovis aries
43	216	13.2	267	6	O02764	O02764 oryctolagus
44	202	12.4	132	13	Q90Y18	Q90y18 salvelinus
45	200	12.2	167	12	Q9DJL2	Q9djl2 cowpox viru

ALIGNMENTS

RESULT 1
Q90W71
ID Q90W71 PRELIMINARY; PRT; 285 AA.
AC Q90W71;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative decoy receptor 3 protein.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEAD KIDNEY;
RA Pleguezuelos O., Secombes C.J.;
RT "Screening a rainbow trout (Oncorhynchus mykiss) cDNA library.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ315137; CAC43329.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 285 AA; 31642 MW; FB75CFFC1E391AD0 CRC64;

Query Match 30.6%; Score 500; DB 13; Length 285;
Best Local Similarity 36.8%; Pred. No. 1.4e-35;
Matches 105; Conservative 42; Mismatches 122; Indels 16; Gaps 6;

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Qy          14 LVLAL-PALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGP 72
               || ||    :||      | |||| ||| ||: | |  | |||:: : | :|  : |||
Db          12 LVFALCGGSVPVSG----AHTPTYIWRDDATGDSLTCDLCAPGTYLLKHCTKDRKSDCGP 67

Qy          73 CPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASC 132
               ||  |||: |||:|||:|||  |   | |:  |   ||| | |: ||:   | |  |  |
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```
Db         68 CPKSHYTEIWNYIERCQYCNRFCTADEIESVPCTQLHNRQCECKDGFYMTHGSCSRHRRC 127

Qy        133 PPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTL 192
              ||| |||: ||   : :|:||| | ||| ||| : ||    |   |    :||:  :|
Db        128 PPGEGVISNGTAHTDVKCEPCPVGFFSAVSSSRKACQKFSVCPPGG--TTIPGNDMNDVY 185

Qy        193 CTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAA 252
              |::||    |    |   |:  :::|:: | :: :: :||:  |    |   |      |
Db        186 CSACTNG--SRTHEGEAICDGELMEFLSLQILTPRKDKRLVAVLRRSAGKATT----NNA 239

Qy        253 LQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFL 297
                | | : :    |       ::   |   |:  |   | : ||
Db        240 TVLDLLKTIKNKAGKH---FAIQMRDILNTDRLLHLRTKVNKWFL 281


RESULT 2
Q90YS6
ID   Q90YS6      PRELIMINARY;      PRT;   285 AA.
AC   Q90YS6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   TNF decoy receptor.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liu L., Fujiki K., Dixon B., Sundick R.S.;
RT   "Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine
RT   with a fractalkine-like stalk and a TNF decoy receptor using cDNA
RT   fragments containing AU-rich elements.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF401631; AAK91758.1; -.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00181; EGF; 1.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   285 AA;  31795 MW;  5E3BD1B6EFC6BABC CRC64;

  Query Match             29.8%;  Score 487;  DB 13;  Length 285;
  Best Local Similarity   36.1%;  Pred. No. 1.9e-34;
  Matches  103;  Conservative   42;  Mismatches  124;  Indels   16;  Gaps    6;

Qy         14 LVLAL-PALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGP 72
              || ||    :||      | |||| |||  ||: | |  | |||:: : | :|  : |||
Db         12 LVFALCGGSVPVSG----AHTPTYIWRDDATGDSLTCDLCAPGTYLLKHCTKDRKSDCGP 67

Qy         73 CPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASC 132
              ||  |||: |||:|||:|||  |   | |:  |   ||| | |: ||:   | |  |  |
Db         68 CPKSHYTEIWNYIERCQYCNRFCTADEIESVPCTQLHNRQCECKDGFYMTHGSCSRHRRC 127

Qy        133 PPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTL 192
              ||| |||: ||   : :|:||| | ||| ||| : ||    |        :||:  :|
Db        128 PPGEGVISNGTAHTDVKCEPCPVGFFSAVSSSRKACQKFSVCPP--GRTTIPGNDMNDVY 185

Qy        193 CTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAA 252
              |::|     |    |   |:  :::|:: | :: :: :||:  |    |   |      |
Db        186 CSACRNG--SRTHEGQAICDGELMEFLSLQILTPRKDKRLVAVLRRSAGKATT----NNA 239

Qy        253 LQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFL 297
                | | : :    |       ::   |   |:  |   | : ||
Db        240 TVLDLLKTIKNKAGKH---FAIQMRDILNTDRLLHLRTKVNKWFL 281


RESULT 3
Q9PUS0
ID   Q9PUS0      PRELIMINARY;      PRT;   302 AA.
AC   Q9PUS0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Decoy TNF receptor.
OS   Salvelinus fontinalis (Brook trout) (Brook char).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX   NCBI_TaxID=8038;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20111091; PubMed=10642582;
RA   Bobe J., Goetz F.W.;
RT   "A tumor necrosis factor decoy receptor homologue is up-regulated in
RT   the brook trout (Salvelinus fontinalis) ovary at the completion of
RT   ovulation.";
RL   Biol. Reprod. 62:420-426(2000).
DR   EMBL; AF156738; AAD56428.1; -.
DR   HSSP; O14763; 1D4V.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   302 AA;  34037 MW;  E44C73477F05C3DF CRC64;

  Query Match             24.2%;  Score 395;  DB 13;  Length 302;
  Best Local Similarity   34.3%;  Pred. No. 1.9e-26;
  Matches   82;  Conservative   44;  Mismatches  101;  Indels   12;  Gaps    7;

Qy         35 TYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVL 94
              |:   |  :|  :|| :|||||::: ||     : |  ||   ||:|||:: :|  |: :
Db         22 TFKNDDRYSGLSIVCDRCPPGTYLRAPCSAMRKSDCAECPNGAYTEFWNHISKCLRCS-M 80

Qy         95 CGEREEEARACHATHNRACRCRTGFFAHAGF--CLEHASCPPGAGVIAPGTPSQNTQCQP 152
              | | :   : |  ::|  | |: |:: :  :  |::|  |||| |    ||| |:|:|
Db         81 CAENQVVKQECSPSNNCECECKEGYYFNKKYEACIKHKECPPGYGANTTGTPHQDTECVQ 140

Qy        153 CPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECE 212
              |  | :|  ||:   |    ||   || : : |   |:||| ||  : | ||  |||
Db        141 CQAGFYSEVSSAKATCLAQSNCKVGGLRVVLKGQDWHNTLCASC--YDLKTR-DGAEYLH 197

Qy        213 RAVIDFV--AFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
                  :  |     | : |||::||  |:  |:  |  |  |  |:  : || | : : |
Db        198 EILPTFFIQLHQTMGIKRMRRL--AMRLPQEGGKKPLIG--AVMKRNRRGLHDFMNSWD 252


RESULT 4
Q62327
ID   Q62327      PRELIMINARY;      PRT;   459 AA.
AC   Q62327;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Murine tumour necrosis factor receptor 2 protein (Fragment).
GN   TNFRSF1B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD;
RA   Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT   "Amino acid variation in the tumor Necrosis factor receptor 2 is
RT   linked to autoimmune diabetes in NOD mice.";
RL   Genomics 0:0-0(0).
RN   [2]
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RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD;
RX   MEDLINE=95178848; PubMed=7873884;
RA   Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT   "Allelic variation of the type 2 tumor necrosis factor receptor
RT   gene.";
RL   Mamm. Genome 5:726-727(1994).
DR   EMBL; X76401; CAA53981.1; -.
DR   HSSP; P19438; 1NCF.
DR   MGD; MGI:1314883; Tnfrsf1b.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor.
FT   NON_TER       1      1
FT   VARIANT      87     87       S -> T.
FT   VARIANT      93     93       T -> I.
FT   VARIANT     268    268       F -> I.
FT   VARIANT     345    345       S -> F.
FT   VARIANT     421    421       Y -> C.
SQ   SEQUENCE   459 AA;  48686 MW;  6C51D2CF1C4626DF CRC64;

  Query Match             20.4%;  Score 333.5;  DB 11;  Length 459;
  Best Local Similarity   29.7%;  Pred. No. 6.4e-21;
  Matches   81;  Conservative   43;  Mismatches  110;  Indels   39;  Gaps    9;

Qy         46 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC 105
              :: ||:|||| :|:  | : | | |  |    ||| ||    |  |:  |   : | |||
Db         37 QMCCAKCPPGQYVKHFCNKTSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRAC 96

Qy        106 HATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 158
                 || | |  | :      |:|    |:  : | || || :   |: |  |: | ||||
Db         97 TKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCKACAPGTF 156

Qy        159 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPGAEECERA 214
              | ::||:: |:||| |: |     :||::| | :|     : :  | :  |   |
Db        157 SDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQPEPTRSQ 212

Qy        215 VIDFVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLTELLGAQD 269
               :|    |:    :  :| :|      | ||       |  :| : |   :| |
Db        213 PLD----QEPGPSQTPSILTSL------GSTPIIEQSTKGGISLPIGLIVGVTSL----- 257

Qy        270 GALLVRLLQAL----RVARMPGLERSVRERFLP 298
              | |:: |:       |  :   |:|  :   :|
Db        258 GLLMLGLVNCFILVQRKKKPSCLQRDAKVPHVP 290


RESULT 5
O88734
ID   O88734      PRELIMINARY;      PRT;   482 AA.
AC   O88734;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   P80 TNF-alpha receptor.
GN   TNFR2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98414512; PubMed=9740674;
RA   Hurle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT   "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
RT   and Characterization of the two Transcripts.";
RL   Genomics 52:79-98(1998).
DR   EMBL; Y14619; CAA74969.1; -.
DR   EMBL; Y14620; CAA74969.1; JOINED.
DR   EMBL; Y14621; CAA74969.1; JOINED.
DR   EMBL; Y14622; CAA74969.1; JOINED.
DR   EMBL; Y14623; CAA74969.1; JOINED.
DR   EMBL; Y14679; CAA74969.1; JOINED.
DR   HSSP; P19438; 1NCF.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor.
SQ   SEQUENCE   482 AA;  51106 MW;  F6C15046B48FF83C CRC64;

  Query Match             20.0%;  Score 327;  DB 11;  Length 482;
  Best Local Similarity   29.3%;  Pred. No. 2.5e-20;
  Matches   82;  Conservative   43;  Mismatches  109;  Indels   46;  Gaps   10;

Qy         46 RLVCAQCPPGTFVQRPCRR-------DSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGER 98
              :: ||:|||| :|:  | :        || | |  |    ||| ||    |  |:  |
Db         52 QMCCAKCPPGQYVKHFCNKTSDTVCADSDTVCADCEASMYTQVWNQFRTCLSCSSSCSTD 111

Qy         99 EEEARACHATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPGTPSQNTQCQ 151
              : | |||    || | |  | :     |:|    |:  : | || || :   |: |  |:
Db        112 QVETRACTKQQNRVCACEAGRYCALKTHSGSCRQCMRLSKCGPGFGVASSRAPNGNVLCK 171

Qy        152 PCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCT----SCTGFPLSTRVPG 207
               | ||||| ::||:: |:||| |: |     :||::| | :|     : :  | :  |
Db        172 ACAPGTFSDTTSSTDVCRPHRICSILA----IPGNASTDAVCAPESPTLSAIPRTLYVSQ 227

Qy        208 AEECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTP-----RAGRAALQLKLRRRLT 262
               |      :|    |:    :  :| :|      | ||       |  :| : |   :|
Db        228 PEPTRSQPLD----QEPGPSQTPSILTSL------GSTPIIEQSTKGGISLPIGLIVGVT 277

Qy        263 ELLGAQDGALLVRLLQAL----RVARMPGLERSVRERFLP 298
               |     | |:: |:       |  :   |:|  :   :|
Db        278 SL-----GLLMLGLVNCFILVQRKKKPSCLQRDAKVPHVP 312


RESULT 6
Q91ZM6
ID   Q91ZM6      PRELIMINARY;      PRT;   433 AA.
AC   Q91ZM6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Tumor necrosis factor receptor type II (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RA   Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT   "TNF-receptors p60 and p80 are constitutively expressed by rat brain
RT   capillary endothelial cells and participate in TNF-alpha transport
RT   through the blood-brain barrier.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF420214; AAL16021.1; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER     433    433
SQ   SEQUENCE   433 AA;  45723 MW;  75736D835E72CA4A CRC64;

  Query Match             19.2%;  Score 313.5;  DB 11;  Length 433;
  Best Local Similarity   35.1%;  Pred. No. 3.3e-19;
  Matches   59;  Conservative   29;  Mismatches   67;  Indels   13;  Gaps    4;

Qy         46 RLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARAC 105
              :: ||:|||| : :  | : | | |  |    :|| ||:|  |  |:  | : : |   |
Db         32 QMCCAKCPPGQYAKHFCNKTSDTVCADCAAGMFTQVWNHLHTCLSCSSSCSDDQVETHNC 91
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Qy        106 HATHNRACRCRTGFFA----HAG---FCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTF 158
                  || | |    :     |:|    |:: : | || ||    | : |  |  | ||||
Db         92 TKKQNRVCACNADSYCALKLHSGNCRQCMKLSKCGPGFGVARSRTSNGNVICSACAPGTF 151

Qy        159 SASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVP 206
              | ::||:: |:||| |: |     :||::| | :| | :  |  : ||
Db        152 SDTTSSTDVCRPHRICSILA----IPGNASTDAVCASES--PTPSAVP 193


RESULT 7
Q98SM6
ID   Q98SM6      PRELIMINARY;      PRT;   651 AA.
AC   Q98SM6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Death receptor 6.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bridgham J.T., Johnson A.L.;
RT   "Expression of DR6 in the ovary.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF349908; AAK29666.2; -.
DR   HSSP; P19438; 1NCF.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR003975; Shal_channel.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00531; death; 1.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   PRINTS; PR01497; SHALCHANNEL.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor.
SQ   SEQUENCE   651 AA;  71003 MW;  BDC95A600DAB2C2A CRC64;

  Query Match             18.0%;  Score 293.5;  DB 13;  Length 651;
  Best Local Similarity   30.8%;  Pred. No. 2.7e-17;
  Matches   61;  Conservative   30;  Mismatches   92;  Indels   15;  Gaps    1;

Qy         18 LPALLPVPAVRGVAETP--------------TYPWRDAETGERLVCAQCPPGTFVQRPC 62
              | |:||:    | |:                  |   |  | : |:| :|| ||:| : |
Db          6 LAAVLPLLVFLGTADAQPKLTSEQNAVSLPAGKYLHLDRATNQELICDKCPAGTYVSKHC 65

Qy         63 RRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAH 122
                : :   | |||   :|:  | :|||  |   |     |   | |  :| | | :| |
Db         66 TKSTLRECSPCPDGTFTKHENGIERCHPCRKPCELPMIEKTHCTALTDRECTCLSGTFQI 125

Qy        123 AGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALN 182
                |: :  || | ||   || ::: :|:||  ||||   ||  :|: : :|    : :
Db        126 NDTCVPYTVCPVGWGVRKKGTETEDVRCKPCLRGTFSDVPSSVMKCKTYTDCFGKNMVVV 185

Qy        183 VPGSSSHDTLCTSCTGFP 200
              ||:   | :| |   |
Db        186 KPGTKESDNVCGSPASLP 203


RESULT 8
O57277
ID   O57277      PRELIMINARY;      PRT;   348 AA.
AC   O57277;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog (J2R) (J2L).
GN   CRMB OR J2R OR J2L.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1996 /96-17, AND ZAIRE-1996 / 96-16;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-96-I-16;
RX   MEDLINE=21592287; PubMed=11734207;
RA   Shchelkunov S.N., Totmenin A.V., Babkin I.V., Safronov P.F.,
RA   Ryazankina O.I., Petrov N.A., Gutorov V.V., Uvarova E.A.,
RA   Mikheev M.V., Sisler J.R., Esposito J.J., Jahrling P.B., Moss B.,
RA   Sandakhchiev L.S.;
RT   "Human monkeypox and smallpox viruses: genomic comparison.";
RL   FEBS Lett. 509:66-70(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-96-I-16;
RA   Shchelkunov S.N., Totmenin A.V., Safronov P.F., Gutorov V.V.,
RA   Ryazankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A.,
RA   Esposito J.J., Moss B., Sisler J.R., Jahrling P.B., Sandakhchiev L.S.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88543; AAB94378.1; -.
DR   EMBL; U87841; AAB94358.1; -.
DR   EMBL; AF380138; AAL40648.1; -.
DR   EMBL; AF380138; AAL40460.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   348 AA;  38212 MW;  54019521556C2D8F CRC64;

  Query Match             17.3%;  Score 282.5;  DB 12;  Length 348;
  Best Local Similarity   30.9%;  Pred. No. 1.3e-16;
  Matches   64;  Conservative   33;  Mismatches   97;  Indels   13;  Gaps    3;

Qy          9 LSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPT 68
              | | |:::   | |     |  :   |  |:      | |  |||||:  | |   : |
Db         10 LFLSCIIINGRDLAPHAPSNGKCKDNEYRSRN------LCCLSCPPGTYASRLCDSKTNT 63

Qy         69 TCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF------AH 122
                | ||    :|   |:|: |  ||  |   : | |:|: |||| | |  |::     :
Db         64 QCTPCGSDTFTSHNNHLQACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGSSG 123

Qy        123 AGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALN 182
                |:    |  | || :  | : :  | || |||:| : ||:::|:|  : |   : :
Db        124 CRTCISKTKCGIGYGV-SGYTSTGDVICSPCGPGTYSHTVSSTDKCEPVTSNTFNYIDVE 182

Qy        183 VPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              :    :|| ||  |   ||  :  :|
Db        183 INLYPVNDTSCTRTTTTGLSESISTSE 209


RESULT 9
O57103
ID   O57103      PRELIMINARY;      PRT;   348 AA.
AC   O57103;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1979;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87847; AAB94364.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   348 AA;  38184 MW;  34A5E668B27907B5 CRC64;

  Query Match             17.2%;  Score 280.5;  DB 12;  Length 348;
  Best Local Similarity   30.4%;  Pred. No. 1.9e-16;
  Matches   63;  Conservative   34;  Mismatches   97;  Indels   13;  Gaps    3;

Qy          9 LSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPT 68
              | | |:::    : |      |  :   |  |:       | |  |||||:  | |   : |
Db         10 LFLSCIIINGRDIAPHAPSNGKCKDNEYRSRN------LCCLSCPPGTYASRLCDSKTNT 63

Qy         69 TCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF------AH 122
                | ||    :|   |:|: |  ||  |   : | |:|: |||| | |  |::      :
Db         64 QCTPCGSDTFTSHNNHLQACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGSSG 123

Qy        123 AGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALN 182
                |:    |  | || :  | : :  | || |||:| : ||:::|:|  : |   : :
Db        124 CRTCISKTKCGIGYGV-SGYTSTGDVICSPCGPGTYSHTVSSTDKCEPVTSNTFNYIDVE 182

Qy        183 VPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              :     :|| ||  |   ||  :  :|
Db        183 INLYPVNDTSCTRTTTTGLSESISTSE 209


RESULT 10
O57108
ID   O57108      PRELIMINARY;      PRT;   348 AA.
AC   O57108;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1970;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88142; AAB94367.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   348 AA;  38212 MW;  E555979057DEC91F CRC64;

  Query Match             17.2%;  Score 280.5;  DB 12;  Length 348;
  Best Local Similarity   30.4%;  Pred. No. 1.9e-16;
  Matches   63;  Conservative   34;  Mismatches   97;  Indels   13;  Gaps    3;

Qy          9 LSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPT 68
              | | |:::    : |      |  :   |  |:       | |  |||||:  | |   : |
Db         10 LFLSCIIINGRDIAPHAPSNGKCKDNEYRSRN------LCCLSCPPGTYASRLCDSKTNT 63

Qy         69 TCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF------AH 122
                | ||    :|   |:|: |  ||  |   : | |:|: |||| | |  |::      :
Db         64 QCTPCGSDTFTSHNNHLQACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGSSG 123

Qy        123 AGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALN 182
                |:    |  | || :  | : :  | || |||:| : ||:::|:|  : |   : :
Db        124 CRTCISKTKCGIGYGV-SGYTSTGDVICSPCGPGTYSHTVSSTDKCEPVTSNTFNYIDVE 182

Qy        183 VPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              :     :|| ||  |   ||  :  :|
Db        183 INLYPVNDTSCTRTTTTGLSESISTSE 209


RESULT 11
O57100
ID   O57100      PRELIMINARY;      PRT;   349 AA.
AC   O57100;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NIGERIA-1971;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87844; AAB94361.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38239 MW;  DF6C280D478F2422 CRC64;

  Query Match             16.9%;  Score 276;  DB 12;  Length 349;
  Best Local Similarity   30.0%;  Pred. No. 4.6e-16;
  Matches   63;  Conservative   34;  Mismatches   95;  Indels   18;  Gaps    5;

Qy          9 LSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPT 68
              | | |:::    : |      |  :   |  |:       | |  |||||:  | |   : |
Db         10 LFLSCIIINGRDIAPHAPSNGKCKDNEYRSRN------LCCLSCPPGTYASRLCDSKTNT 63

Qy         69 TCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF------AH 122
                | ||    :|   |:|: |  ||  |   : | |:|: |||| | |  |::      :
Db         64 QCTPCGSDTFTSHNNHLQACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGASG 123

Qy        123 AGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQP---HRNCTALGL 179
                |:    |  | || :  | : :  | || |||:| : ||:::|:|        : :
Db        124 CSTCISKTKCGIGYGV-SGYTSTGDVICSPCGPGTYSHTVSSTDKCEPVVTSNTFNYIDV 182

Qy        180 ALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              :|:     :|| ||  |   ||  :  :|
Db        183 EINL--YPVNDTSCTRTTTTGLSESISTSE 210


RESULT 12
O57101
ID   O57101      PRELIMINARY;      PRT;   349 AA.
AC   O57101;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
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```
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1977;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87845; AAB94362.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38311 MW;  02F65B00CFB858BE CRC64;

  Query Match             16.8%;  Score 274;  DB 12;  Length 349;
  Best Local Similarity   30.0%;  Pred. No. 6.9e-16;
  Matches   63;  Conservative   34;  Mismatches   95;  Indels   18;  Gaps    5;

Qy          9 LSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPT 68
              | | |:::    : |     |  :   |  |:      | |  |||||:  | |   : |
Db         10 LFLSCIIINGRDIAPHAPSNGKCKDNEYRSRN------LCCLSCPPGTYASRLCDSKTNT 63

Qy         69 TCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF------AH 122
                | ||    :|   |:|: |  ||  |   : | |:|: |||| | |  |::      :
Db         64 QCTPCGSDTFTSHNNHLQACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGSSG 123

Qy        123 AGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQP---HRNCTALGL 179
                |:    |  | || :  | : :  | || |||:| : ||:::|:|         : :
Db        124 CRTCISKTKCGIGYGV-SGYTSTGDVICSPCGPGTYSHTVSSTDKCEPVVTSNTFNYIDV 182

Qy        180 ALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
                :|:     :|| ||  |   ||  :  :|
Db        183 EINL--YPVNDTSCTRTTTTGLSESISTSE 210


RESULT 13
O57102
ID   O57102      PRELIMINARY;      PRT;   349 AA.
AC   O57102;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BENIN-1978;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87846; AAB94363.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38308 MW;  CBD2C949F994C59C CRC64;

  Query Match             16.8%;  Score 274;  DB 12;  Length 349;
  Best Local Similarity   30.0%;  Pred. No. 6.9e-16;
  Matches   63;  Conservative   34;  Mismatches   95;  Indels   18;  Gaps    5;

Qy          9 LSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPT 68
              | | |:::    : |     |  :   |  |:      | |  |||||:  | |   : |
Db         10 LFLSCIIINGRDIAPHAPSNGKCKDNEYRSRN------LCCLSCPPGTYASRLCDSKTNT 63

Qy         69 TCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF------AH 122
                | ||    :|   |:|: |  ||  |   : | |:|: |||| | |  |::      :
Db         64 QCTPCGSDTFTSHNNHLQACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGASG 123

Qy        123 AGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQP---HRNCTALGL 179
                |:    |  | || :  | : :  | || |||:| : ||:::|:|         : :
Db        124 CRTCISKTKCGIGYGV-SGYTSTGDVICSPCGPGTYSHTVSSTDKCEPVVTSNTFNYIDV 182

Qy        180 ALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
                :|:     :|| ||  |   ||  :  :|
Db        183 EINL--YPVNDTSCTRTTTTGLSESISTSE 210


RESULT 14
O57291
ID   O57291      PRELIMINARY;      PRT;   349 AA.
AC   O57291;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VARIOUS STRAINS;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88144; AAB94369.1; -.
DR   EMBL; U87842; AAB94359.1; -.
DR   EMBL; U87994; AAB94365.1; -.
DR   EMBL; U87995; AAB94366.1; -.
DR   EMBL; U88143; AAB94368.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   349 AA;  38295 MW;  CBD2C949ED2B8E7C CRC64;

  Query Match             16.8%;  Score 274;  DB 12;  Length 349;
  Best Local Similarity   30.0%;  Pred. No. 6.9e-16;
  Matches   63;  Conservative   34;  Mismatches   95;  Indels   18;  Gaps    5;

Qy          9 LSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPT 68
              | | |:::    : |     |  :   |  |:      | |  |||||:  | |   : |
Db         10 LFLSCIIINGRDIAPHAPSNGKCKDNEYRSRN------LCCLSCPPGTYASRLCDSKTNT 63

Qy         69 TCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF------AH 122
                | ||    :|   |:|: |  ||  |   : | |:|: |||| | |  |::      :
Db         64 QCTPCGSDTFTSHNNHLQACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGASG 123

Qy        123 AGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQP---HRNCTALGL 179
                |:    |  | || :  | : :  | || |||:| : ||:::|:|         : :
Db        124 CRTCISKTKCGIGYGV-SGYTSTGDVICSPCGPGTYSHTVSSTDKCEPVVTSNTFNYIDV 182

Qy        180 ALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
                :|:     :|| ||  |   ||  :  :|
Db        183 EINL--YPVNDTSCTRTTTTGLSESISTSE 210
```

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RESULT 15
O57099
ID   O57099      PRELIMINARY;      PRT;   349 AA.
AC   O57099;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Tumor necrosis factor receptor II homolog.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SIERRA LEONE-1970;
RA   Loparev V.N., Parsons J.M., Esposito J.J.;
RT   "DNA sequence analysis as a criterion for allocation of the
RT   orthopoxviruses to a particular species.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87843; AAB94360.1; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
SQ   SEQUENCE   349 AA;  38321 MW;  FE449028CC933F57 CRC64;

  Query Match             16.7%;  Score 273;  DB 12;  Length 349;
  Best Local Similarity   30.0%;  Pred. No. 8.4e-16;
  Matches   63;  Conservative   33;  Mismatches   96;  Indels   18;  Gaps    5;

Qy          9 LSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPT 68
              | | |:::    : |     |  :   |  |:      | |  |||||:  | |   : |
Db         10 LFLSCIIINGRDIAPHAPSNGKCKDNEYRSRN------LCCLSCPPGTYASRLCDSKTNT 63

Qy         69 TCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFFA------H 122
               | ||    :|   |:|: |  ||  |   : | |:|: |||| | |  |::
Db         64 QCTPCGSDTFTSHNNHLQACLSCNGRCDSNQVETRSCNTTHNRICECSPGYYCLLKGALG 123

Qy        123 AGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQP---HRNCTALGL 179
                :|    |  | || :  | : :  | || |||:| : ||:::|:|         : :
Db        124 CRTCISKTKCGIGYGV-SGYTSTGDVICSPCGPGTYSHTVSSTDKCEPVVTSNTFNYIDV 182

Qy        180 ALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              :|:     :|| ||  |   ||  :  :|
Db        183 EINL--YPVNDTSCTRTTTGLSESISTSE 210


Search completed: July 16, 2003, 19:38:58
Job time : 83 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 16, 2003, 19:37:04 ; Search time 38 Seconds
(without alignments)
1051.979 Million cell updates/sec

Title: US-09-935-727-2
Perfect score: 300
Sequence: 1 MRALEGPGLSLLCLVLALPA.....RVARMPGLERSVRERFLPVH 300

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_101002:*
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22: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	300	100.0	300	19	AAW66102	Amino acid sequenc
2	300	100.0	300	19	AAW63622	Human tumour necro
3	300	100.0	300	20	AAY03099	Human lung TNF-rec
4	300	100.0	300	20	AAY42182	Human FLINT #1 pro
5	300	100.0	300	20	AAY17479	Mammalian tumour n
6	300	100.0	300	20	AAY06817	Human DcR3 polypep
7	300	100.0	300	20	AAW97749	Human tumour necro
8	300	100.0	300	20	AAW95082	Orphan receptor (H
9	300	100.0	300	21	AAB19335	A full length huma
10	300	100.0	300	21	AAB28559	Human soluble TNF
11	300	100.0	300	21	AAB24057	Human PRO212 prote
12	300	100.0	300	21	AAB33416	Human PRO212 prote
13	300	100.0	300	21	AAB03621	Human Fas ligand i
14	300	100.0	300	21	AAY97246	M68 TNF receptor r
15	300	100.0	300	21	AAY90357	Human tumour necro
16	300	100.0	300	21	AAB24395	Human PRO212 prote
17	300	100.0	300	21	AAY96596	Human FLINT. Homo
18	300	100.0	300	22	AAE03568	Human native fas l
19	300	100.0	300	22	AAB74466	Human FLINT native
20	300	100.0	300	22	AAB71754	Human NTR3. Homo
21	300	100.0	300	22	AAB48161	Human PRO212 polyp
22	300	100.0	300	22	AAB50903	Human PRO212 prote
23	300	100.0	300	23	AAE14579	Human native FLINT
24	300	100.0	300	23	AAE20848	Human tumour necro
25	300	100.0	341	22	AAG73740	Human colon cancer
26	279	93.0	326	23	ABP41980	Human ovarian anti
27	271	90.3	271	20	AAY42184	Human mFLINT #1 pr
28	271	90.3	271	21	AAB19334	A mature human FAS
29	271	90.3	271	21	AAB19705	Human FAS ligand i
30	271	90.3	271	21	AAY97247	M68 TNF receptor r
31	271	90.3	271	21	AAY96598	Human mature FLINT
32	271	90.3	271	22	AAE03567	Human mature fas l
33	271	90.3	271	22	AAB68044	Amino acid sequenc
34	271	90.3	271	22	AAB68047	Amino acid sequenc
35	271	90.3	271	22	AAB74465	Human FLINT mature
36	271	90.3	271	23	AAE14578	Human mature FLINT
37	240	80.0	245	20	AAY28449	A human tumour nec
38	217	72.3	271	21	AAB19709	Protease-resistant
39	217	72.3	271	22	AAE03571	Human mature fas l
40	217	72.3	271	22	AAE03584	Human mature fas l
41	217	72.3	271	22	AAB74467	Human FLINT mature
42	217	72.3	271	23	AAE14581	Human protease-res
43	217	72.3	271	23	AAE14582	Human protease-res
44	217	72.3	271	23	AAE14584	Human protease-res
45	217	72.3	271	23	AAE14585	Human protease-res

ALIGNMENTS

RESULT 1
AAW66102
ID AAW66102 standard; Protein; 300 AA.
XX
AC AAW66102;
XX
DT 02-DEC-1998 (first entry)
XX
DE Amino acid sequence of tumour necrosis related receptor (TR4).
XX
KW Human; tumour necrosis related receptor; TR4; agonist; antagonist;
KW inhibition; chronic; acute; inflammation; arthritis; septicaemia;
KW autoimmune disease; transplant rejection; stroke; cancer;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN EP861850-A1.
XX
PD 02-SEP-1998.
XX
PF 20-JAN-1998; 98EP-0300382.
XX
PR 04-FEB-1997; 97US-0794796.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Emery J, Tan KB, Truneh A, Young PR;
XX
DR WPI; 1998-508248/44.
DR N-PSDB; AAV07654.
XX
PT New DNA encoding tumour necrosis related receptor - used to treat

PT and prevent e.g. inflammation, arthritis, septicaemia, autoimmune
PT diseases, transplant rejection, infection, stroke, ischaemia, ARDS,
PT restenosis, AIDS, bone disorders and cancer
XX
PS Claim 1; Fig 1; 21pp; English.
XX
CC This is the amino acid sequence of the human tumour necrosis related
CC receptor (TR4), used in the method of the invention. The TR4 protein
CC or its agonist can be used to treat a subject in need of enhanced
CC TR4 polypeptide activity. The antagonist is used to inhibit TR4
CC polypeptide activity. The active agents can be used for the
CC treatment and prevention of diseases such as chronic and acute
CC inflammation, arthritis, septicaemia, autoimmune diseases, transplant
CC rejection, stroke, cancer, Alzheimer's disease.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 300; DB 19; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.6e-269;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
Db 1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy 61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
Db 61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy 121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
Db 121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy 181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
Db 181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy 241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
Db 241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300

RESULT 2
AAW63622
ID AAW63622 standard; Protein; 300 AA.
XX
AC AAW63622;
XX
DT 26-OCT-1998 (first entry)
XX
DE Human tumour necrosis factor receptor-6 alpha protein.
XX
KW Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
KW endothelial cells; keratinocytes; normal prostate; apoptosis;
KW prostate tumour tissue.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Protein 31..300
FT /note= "TNFR-6 alpha"
FT Region 31..282
FT /note= "Soluble extracellular domain"
XX
PN WO9830694-A2.
XX
PD 16-JUL-1998.
XX
PF 13-JAN-1998; 98WO-US00153.
XX
PR 14-JAN-1997; 97US-0035496.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;
XX
DR WPI; 1998-399142/34.
DR N-PSDB; AAV39085.
XX
PT Human tumour necrosis factor receptors 6-alpha and 6-beta - used in
PT the diagnosis of immune system-related disorder(s)
XX
PS Claim 20; Fig 1; 91pp; English.
XX
CC The present sequence represents the human tumour necrosis factor
CC receptor-6 alpha (TNFR-6 alpha) protein. The invention also provides
CC for the TNFR-6 beta protein (AAW63623). TNFR-6 alpha and TNFR-6 beta
CC are members of the tumour necrosis factor receptor (TNFR) family. TNFRs
CC are expressed in endothelial cells, keratinocytes, normal prostate and
CC prostate tumour tissue. For a number of disorders of these cells,
CC particularly of the immune system, substantially altered (whether
CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene
CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta
CC polypeptides, nucleic acids and antibodies are claimed to be useful in
CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and
CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are
CC also claimed to be useful for identifying ligands which may be useful
CC in the treatment of apoptosis related disorders.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 300; DB 19; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.6e-269;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
Db 1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy 61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
Db 61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy 121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
Db 121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy 181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
Db 181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy 241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
Db 241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300

RESULT 3
AAY03099
ID AAY03099 standard; Protein; 300 AA.
XX
AC AAY03099;
XX
DT 09-DEC-1999 (first entry)
XX
DE Human lung TNF-receptor protein.
XX
KW Tumour necrosis factor; TNF; TNF receptor; human; lung; gene therapy;
KW detection; immunoassay; diagnosis; disease; immune system; tumour;
KW osteogenic system; cardiovascular system; central nervous system; asthma;
KW peripheral nervous systems; transplant incompatibility; antitumor;
KW rheumatoid arthritis; antiasthmatic; antiarthritic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers

```
FT   CDS             134..1036
FT                   /*tag=  a
FT                   /product= "TNF-receptor"
XX
PN   DE19809978-A1.
XX
PD   16-SEP-1999.
XX
PF   09-MAR-1998;   98DE-1009978.
XX
PR   09-MAR-1998;   98DE-1009978.
XX
PA   (BADI ) BASF AG.
XX
PI   Kroeger B;
XX
DR   WPI; 1999-519473/44.
DR   N-PSDB; AAZ09998.
XX
PT   New soluble member of tumor necrosis factor receptor family, useful for
PT   identification specific modulators and for treating disease e.g. tumors
PT    -
XX
PS   Claim 1; Page 8-9; 10pp; German.
XX
CC   This invention describes a novel tumour necrosis factor (TNF) receptor
CC   (I) isolated from human lung tissue. (I) is used: (i) to raise specific
CC   antibodies (Ab); (ii) to screen for specific (ant)agonists or ligands
CC   (A), potential therapeutic agents; and (iii) therapeutically (optionally
CC   expressed from a gene therapy vector) in conditions associated with a
CC   deficit of (I). Ab are used: (a) for qualitative or quantitative
CC   detection of (I) in standard immunoassays (for diagnosis of disease, or
CC   susceptibility, or for monitoring); and (b) as therapeutic inhibitors in
CC   cases where (I) is overexpressed. Nucleic acid (II) that encodes (I) is
CC   used: (A) for recombinant production of (I); (B) also its oligonucleotide
CC   fragments, in standard hybridization and/or amplification assays; (C) as
CC   source of antisense molecules or ribozymes; and (D) to produce transgenic
CC   animals (for studying (patho)physiology of (I)). Diseases possibly
CC   associated with under- or over-expression of (I) are those of the immune,
CC   osteogenic, cardiovascular and central or peripheral nervous systems,
CC   tumors, transplant incompatibility, asthma and rheumatoid arthritis. The
CC   products of the invention have antitumor, antiasthmatic and
CC   antiarthritic activity. This sequence represents the TNF-receptor of the
CC   invention.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 300;  DB 20;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-269;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300

RESULT 4
AAY42182
ID   AAY42182 standard; Protein; 300 AA.
XX
AC   AAY42182;
XX
DT   17-DEC-1999  (first entry)
XX
DE   Human FLINT #1 protein sequence.
XX
KW   Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
KW   apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW   sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW   reperfusion-associated injury; aplastic anaemia; differentiation;
KW   growth; myelodysplastic syndrome; pancytopenic condition;
KW   myocardial ischaemia.
XX
OS   Homo sapiens.
XX
PN   WO9950413-A2.
XX
PD   07-OCT-1999.
XX
PF   30-MAR-1999;   99WO-US06797.
XX
PR   30-MAR-1998;   98US-0079856.
PR   20-MAY-1998;   98US-0086074.
PR   09-SEP-1998;   98US-0099643.
PR   17-DEC-1998;   98US-0112577.
PR   18-DEC-1998;   98US-0112703.
PR   18-DEC-1998;   98US-0112933.
PR   22-DEC-1998;   98US-0113407.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Bumol TF,  Dou S,  Glasebrook AL,  Gould KE,  Hale JE,  Heuer JG;
PI   Hui KY,  Kharitonenkov A,  Mizrahi J,  Na S,  Noblitt TW,  Reidy CA;
PI   Song HY,  Wang J,  Wu X,  Zuckerman SH;
XX
DR   WPI; 1999-591319/50.
DR   N-PSDB; AAZ25375.
XX
PT   Use of mature FLINT for treating acute liver failure, inflammation,
PT   cancer, and diabetes  - by prevention of FasL-Fas mediated apoptotic
PT   and proinflammatory activity
XX
PS   Claim 30; Fig 1; 99pp; English.
XX
CC   The present invention describes therapeutic applications of mature FLINT
CC   (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
CC   (mFLINT), which is a member of the tumour necrosis factor receptor
CC   superfamily, is used for treating acute liver failure, inflammation of
CC   the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
CC   with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
CC   injury or disorder such as hypercoagulation (including use with
CC   thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
CC   or disorder, Type I diabetes, cancer, cell damage or damage to an
CC   innocent bystander tissue that is induced by a chemotherapeutic agent or
CC   therapeutic irradiation, treating haematopoietic progenitor cells that
CC   have been exposed to therapeutic radiation or chemotherapy, aplastic
CC   anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
CC   also used for promoting the growth or differentiation of a haematopoietic
CC   progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
CC   resulting from abnormal myocardial ischaemia. The present sequence
CC   represents human FLINT.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 300;  DB 20;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-269;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 5
AAY17479
ID   AAY17479 standard; Protein; 300 AA.
XX
AC   AAY17479;
XX
DT   02-AUG-1999  (first entry)
XX
DE   Mammalian tumour necrosis factor receptor OPG-2.
XX
KW   Tumour necrosis factor receptor; TNF receptor; OPG-2; Paget's disease;
KW   osteopenic disorder; osteoclast activity; primary osteoporosis;
KW   hyperglycaemia; osteolytic metastasis; immune response; cancer.
XX
OS   Mammalia.
XX
PN   WO9926977-A1.
XX
PD   03-JUN-1999.
XX
PF   24-NOV-1998;   98WO-US25065.
XX
PR   17-FEB-1998;   98US-0074896.
PR   24-NOV-1997;   97US-0066446.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Tschopp J;
XX
DR   WPI; 1999-347693/29.
DR   N-PSDB; AAX76052.
XX
PT   New tumour necrosis factor family receptor OPG-2
XX
PS   Claim 1; Page 18; 22pp; English.
XX
CC   The present sequence represents a mammalian tumour necrosis factor
CC   receptor, designated OPG-2. OPG-2, is a member of the tumour necrosis
CC   factor receptor family, and can be used: (i) to raise specific
CC   antibodies (Ab), (ii) to treat osteopenic disorders associated with
CC   excessive osteoclast activity, e.g. primary osteoporosis, Paget's
CC   disease, hyperglycaemia of malignancy, or osteolytic metastases; (iii)
CC   for affinity purification of cognate ligands, and (iv) to screen for
CC   ligands (antagonists or agonists). Ab, or other OPG-2 blocking agents
CC   such as soluble forms of the protein, are used to prevent, or reduce
CC   severity of, an immune response, and for treating cancer. They can also
CC   be used in diagnostic assays. The nucleic acid sequence encoding OPG-2
CC   can be used as a probe to isolate related sequences from other species.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 300;  DB 20;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-269;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 6
AAY06817
ID   AAY06817 standard; Protein; 300 AA.
XX
AC   AAY06817;
XX
DT   24-JUN-1999  (first entry)
XX
DE   Human DcR3 polypeptide.
XX
KW   DcR3 polypeptide; tumour necrosis factor receptor; TNFR; Fas ligand;
KW   apoptosis; T cell mediated immune response; allergy; asthma; cancer;
KW   rheumatoid arthritis; Crohn's disease; guest vs. host disease; human;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO9914330-A1.
XX
PD   25-MAR-1999.
XX
PF   18-SEP-1998;   98WO-US19661.
XX
PR   30-JUL-1998;   98US-0094640.
PR   18-SEP-1997;   97US-0059288.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Botstein D,  Dodge KH,  Goddard A,  Gurney AL;
PI   Kim KJ,  Lawrence DA,  Pitti R,  Roy MA,  Tumas DB;
PI   Wood WI;
XX
DR   WPI; 1999-244032/20.
DR   N-PSDB; AAX32744.
XX
PT   DcR3 polypeptide related to tumor necrosis factor receptor
XX
PS   Claim 5; Fig 1; 88pp; English.
XX
CC   This represents a human DcR3 polypeptide, a homologue of tumour necrosis
CC   factor receptor (TNFR) polypeptide. Host cells containing a vector
CC   comprising the DcR3 nucleic acid can be used for the recombinant
CC   expression of the protein. DcR3 binds to Fas ligand, so it (or its
CC   chimeras) are useful for modulating apoptosis in mammalian cells, also
CC   other Fas-ligand induced activities, particularly to inhibit T cell
CC   mediated immune responses, e.g. in treatment of allergy, asthma,
CC   rheumatoid arthritis, Crohn's disease, guest vs. host disease etc. DcR3
CC   may also be used to identify specific binding proteins, potential
CC   inhibitors. Antibodies against DcR3 are used to treat cancer,
CC   specifically of the lung and colon, also in diagnosis and for affinity
CC   purification of the protein. Detecting mutations in the gene for DcR3 is
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CC   also used to diagnose cancer, or predisposition to it. DcR3 nucleic acid
CC   is useful as hybridization probe to detect genomic or related sequences;
CC   for chromosome and gene mapping; as source of antisense sequences; for
CC   expression of recombinant DcR3 and to generate transgenic animals (for
CC   development and screening of therapeutic agents), also for in vivo or
CC   ex vivo gene therapy.
XX
SQ   Sequence   300 AA;

  Query Match            100.0%;  Score 300;  DB 20;  Length 300;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-269;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 7
AAW97749
ID   AAW97749 standard; Protein; 300 AA.
XX
AC   AAW97749;
XX
DT   21-MAY-1999  (first entry)
XX
DE   Human tumour necrosis factor receptor ZTNFR-5.
XX
KW   ZTNFR-5; tumour necrosis factor receptor; TNFR; human;
KW   cell maturation; bone cell regulation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1..23
FT                    /note= "signal peptide"
FT   Protein          24..300
FT                    /note= "mature protein"
FT   Domain           24..194
FT                    /note= "extracellular domain"
FT   Region           49..71
FT                    /note= "cysteine-rich pseudo-repeat 1"
FT   Region           72..113
FT                    /note= "cysteine-rich pseudo-repeat 1"
FT   Region           114..151
FT                    /note= "cysteine-rich pseudo-repeat 1"
FT   Region           152..194
FT                    /note= "cysteine-rich pseudo-repeat 1"
XX
PN   WO9904001-A1.
XX
PD   28-JAN-1999.
XX
PF   21-JUL-1998;   98WO-US15072.
XX
PR   21-JUL-1997;   97US-0053203.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Farrah TM;
XX
DR   WPI; 1999-132245/11.
DR   N-PSDB; AAX07226.
XX
PT   Novel tumour necrosis factor receptor ZTNFR5  - useful for
PT   regulating maturation of TNF-ligand bearing cells
XX
PS   Claim 1; Page 84-85; 109pp; English.
XX
CC   This polypeptide comprises a new, secreted tumour necrosis factor
CC   receptor (see AAW97749), designated ZTNFR-5.  Novel ZTNFR-5 encoding
CC   polynucleotides and polypeptides were initially identified by
CC   querying an expressed sequence tag (EST) database for sequences
CC   homologous to conserved motifs within the TNF receptor family.
CC   Based on this search, a contig of 16 ESTs (see AAX07226) was
CC   constructed.  ZTNFR-5 polypeptides comprise 4 cysteine-rich repeats
CC   (see also AAW97750-55) that are homologous to other TNF receptors, in
CC   particular the soluble, secreted TNF receptor osteoprotegerin.
CC   ZTNFR-5 polypeptide can be prepared by recombinant methods.  The
CC   polypeptide, especially the extracellular domain, can be used to
CC   generate a soluble variant of ZTNFR-5.  The polypeptides and
CC   nucleic acids can be used to screen for ligands, agonists and
CC   antagonists of ZTNFR-5.  The polypeptides can be used in bone cell
CC   regulation and to regulate the maturation of TNF ligand-bearing
CC   cells such as T- or B-cells, lymphocytes, peripheral blood
CC   mononuclear cells, polymorphonuclear leukocytes, fibroblasts or
CC   haematopoietic cells.
XX
SQ   Sequence   300 AA;

  Query Match            100.0%;  Score 300;  DB 20;  Length 300;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-269;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 8
AAW95082
ID   AAW95082 standard; Protein; 300 AA.
XX
AC   AAW95082;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Orphan receptor (HUMAN NTR-1) polypeptide.
XX
KW   HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;
KW   tumour necrosis factor receptor; muscle disorder; bone mass; screening;
KW   muscle metabolism; binding agent; cognate ligand.
XX
OS   Homo sapiens.
```

XX
PN WO9907738-A2.
XX
PD 18-FEB-1999.
XX
PF 04-AUG-1998; 98WO-US16202.
XX
PR 06-AUG-1997; 97US-0054869.
XX
PA (PROC) PROCTER & GAMBLE CO.
PA (REGE-) REGENERON PHARM INC.
XX
PI Masiakowski PJ, Morris J, Valenzuela DM;
XX
DR WPI; 1999-167365/14.
DR N-PSDB; AAX22300.
XX
PT Novel orphan human receptor polypeptide and nucleic acid - useful as
PT diagnostic reagents and for treatment of muscle disorders
XX
PS Claim 7; Page 21; 23pp; English.
XX
CC This represents a HUMAN NTR-1 polypeptide, a novel orphan receptor. The
CC protein is related to osteoprotegerin (OPG) and to tumour necrosis factor
CC receptor (TNFR). Host cells transformed with a vector comprising the
CC HUMAN NTR-1 nucleic acid are used for the recombinant expression of the
CC protein. HUMAN NTR-1 proteins and antibodies immuno specific for the
CC protein are useful for diagnosis and treatment of humans and animals,
CC especially muscle disorders, as the receptor is involved in regulation of
CC bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful
CC for screening for novel binding agents, and cognate ligands, which may be
CC used to treat disorders associated with HUMAN NTR-1 imbalance.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 300; DB 20; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.6e-269;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
```

RESULT 9
AAB19335
ID AAB19335 standard; Protein; 300 AA.
XX
AC AAB19335;
XX
DT 19-FEB-2001 (first entry)
XX
DE A full length human FAS Ligand Inhibitory Protein (FLINT).
XX
KW Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;
KW tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;
KW acute respiratory distress syndrome; ulcerative colitis;
KW chronic obstructive pulmonary disease; Crohn's disease.
XX
OS Homo sapiens.
XX
PN WO200058465-A2.
XX
PD 05-OCT-2000.
XX
PF 20-MAR-2000; 2000WO-US06417.
XX
PR 30-MAR-1999; 99US-0126839.
PR 21-JUN-1999; 99US-0140077.
PR 21-JUN-1999; 99US-0140156.
PR 20-OCT-1999; 99US-0160566.
PR 18-FEB-2000; 2000US-0183398.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JE, Micanovic R;
PI Newton CM, Noblitt TW, Rathmachalam R, Tschang SR, Witcher DR;
PI Wroblewski VJ;
XX
DR WPI; 2000-656167/63.
XX
PT FAS Ligand Inhibitory Protein analogs useful for treating abnormal
PT apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,
PT chronic obstructive pulmonary disease ulcerative colitis or Crohn's
PT disease -
XX
PS Disclosure; Page 113-114; 114pp; English.
XX
CC The present sequence represents a full length human FAS Ligand Inhibitory
CC Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor
CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature
CC FLINT protein is modified to produce analogues, which have greater
CC potency, longer in vivo half-lives, decreased aggregation, decreased
CC absorption onto surfaces, increased solubility and improved ease of
CC formulation. The FLINT analogue is useful for treating a patient
CC suffering from disease or condition relating to abnormal apoptosis such
CC as acute lung injury, acute respiratory distress syndrome, pulmonary
CC fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
CC Crohn's disease.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 300; DB 21; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.6e-269;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
```

RESULT 10
AAB28559
ID AAB28559 standard; protein; 300 AA.

```
XX
AC   AAB28559;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human soluble TNF receptor tnfrGT-1.
XX
KW   Human; tumour necrosis factor like-1; TNFL1; tumour necrosis factor; TNF;
KW   immunosuppressive; antiarthritic; neuroprotective; dermatalogical;
KW   antiinflammatory; antidiabetic; cytostatic; osteopathic; gene therapy;
KW   colon cancer; rheumatoid arthritis; septic shock; Crohn's disease;
KW   osteoporosis; autoimmune disease; myasthenia gravis;
KW   insulin-dependent diabetes mellitus.
XX
OS   Homo sapiens.
XX
PN   WO200060079-A2.
XX
PD   12-OCT-2000.
XX
PF   05-APR-2000; 2000WO-US09058.
XX
PR   05-APR-1999;   99US-0286529.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Tribouley C;
XX
DR   WPI; 2000-665004/64.
DR   N-PSDB; AAC63764.
XX
PT   Tumor necrosis factor (TNF) and TNF receptor superfamily protein
PT   members TNF-L and TNFR-L, useful for enhancing or decreasing TNF
PT   activities such as inducing cell death and lymphoid organogenesis -
XX
PS   Claim 1; Page 72; 77pp; English.
XX
CC   The present sequence is given in a specification relating to an isolated
CC   human protein designated tumour necrosis factor like-1 (TNFL1). It may be
CC   used to induce cell death in tumours, to induce apoptosis of activated T
CC   cells, to induce inflammation, and to rescue resting T cells from
CC   apoptosis. TNF receptors are used to regulate the function of a TNF
CC   ligand which plays a role in apoptosis, inflammation, differentiation, or
CC   proliferation. Expression of the receptors can also be useful as markers
CC   for cancer, especially for colon cancer. Diseases which can be treated
CC   using ligands and/or receptors of the TNF/TNFR superfamily include
CC   rheumatoid arthritis, cancer, septic shock, Crohn's disease and
CC   osteoporosis. The polynucleotides can be used in gene delivery vehicles,
CC   for the purpose of delivering a mRNA or oligonucleotide, full-length
CC   protein, fusion protein, polypeptide, or ribozyme, or single-chain
CC   antibody, into a cell. The newly identified receptor proteins play
CC   regulatory roles in cell proliferation and/or differentiation. The
CC   receptors can also play a role in the negative regulation of
CC   osteoclastogenesis. Soluble TNFR-like receptors can be useful in the
CC   neutralisation of TNF or TNF-like ligands. A TNF-L protein can also be
CC   used to treat autoimmune diseases (myasthenia gravis and
CC   insulin-dependent diabetes mellitus), tumours, and proliferative
CC   disorders. A TNF-L or TNFR-L subgenomic polynucleotide can also be
CC   delivered to subjects for the purpose of screening test compounds for
CC   those which are useful for enhancing transfer of TNF-L subgenomic
CC   polynucleotides to the cell or for enhancing subsequent biological
CC   effects of TNF-L or TNFR-L subgenomic polynucleotides within the cell.
XX
SQ   Sequence   300 AA;

  Query Match           100.0%;  Score 300;  DB 21;  Length 300;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-269;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 11
AAB24057
ID   AAB24057 standard; Protein; 300 AA.
XX
AC   AAB24057;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human PRO212 protein sequence SEQ ID NO:2.
XX
KW   Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW   proliferation; tumourigenesis; identification; cancer; cytostatic;
KW   nootropic; neuroprotective; antiinflammatory; immunosuppressive;
KW   immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW   neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
KW   hypothalamic disorder; glandular disorder; macrophagal disorder;
KW   epithelial disorder; stromal disorder; blastocoelic disorder;
KW   inflammatory disorder; immunologic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200053755-A2.
XX
PD   14-SEP-2000.
XX
PF   06-JAN-2000; 2000WO-US00376.
XX
PR   08-MAR-1999;   99WO-US05028.
PR   02-JUN-1999;   99WO-US12252.
PR   23-JUN-1999;   99US-0141037.
PR   07-JUL-1999;   99US-0143048.
PR   26-JUL-1999;   99US-0145698.
PR   30-NOV-1999;   99WO-US28313.
PR   20-DEC-1999;   99WO-US30911.
PR   05-JAN-2000; 2000WO-US00219.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Goddard A,  Gurney AL,  Hillan KJ,  Roy MA;
PI   Watanabe CK,  Wood WI;
XX
DR   WPI; 2000-572270/53.
DR   N-PSDB; AAC58367.
XX
PT   Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT   treatment, diagnosis and prevention of cancer -
XX
PS   Claim 61; Fig 2; 286pp; English.
XX
CC   The present invention describes an isolated antibody  that binds to
CC   one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
CC   PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
CC   PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
CC   PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
CC   PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
CC   growth. The PRO polypeptides and nucleotides are useful in the
```

```
CC   treatment, diagnosis and prevention of cancer. The antibodies and other
CC   anti-tumour compounds maybe used to treat various conditions, including
CC   those characterised by overexpression and/or activation of the amplified
CC   PRO genes. Exemplary conditions or disorders to be treated with such
CC   antibodies and other compounds include benign or malignant tumours.
CC   (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
CC   colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
CC   carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
CC   leukaemias and lymphoid malignancies, other disorders such as neuronal,
CC   glial, astrocytal, hypothalamic and other glandular, macrophagal,
CC   epithelial, stromal and blastocoelic disorders, and inflammatory,
CC   angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
CC   primers and hybridisation probes used in the isolation of the human PRO
CC   sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
CC   PRO polynucleotide and protein sequences given in the exemplification of
CC   the present invention.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 300;  DB 21;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-269;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 12
AAB33416
ID   AAB33416 standard; Protein; 300 AA.
XX
AC   AAB33416;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human PRO212 protein UNQ186 SEQ ID NO:14.
XX
KW   Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW   dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW   haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW   antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW   antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW   osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW   idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW   systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW   autoimmune thrombocytopaenia; immune-mediated renal disease;
KW   demyelinating disease; hepatobiliary disease; Whipple's disease;
KW   inflammatory bowel disease; gluten-sensitive enteropathy;
KW   autoimmune disease; immune-mediated skin disease; allergic disease;
KW   immunological disease; transplantation associated disease;
KW   graft rejection; graft-versus-host-disease.
XX
OS   Homo sapiens.
XX
PN   WO200053758-A2.
XX
PD   14-SEP-2000.
XX
PF   02-MAR-2000; 2000WO-US05841.
XX
PR   08-MAR-1999;   99WO-US05028.
PR   10-MAR-1999;   99US-0123618.
PR   12-MAR-1999;   99US-0123957.
PR   23-MAR-1999;   99US-0125775.
PR   12-APR-1999;   99US-0128849.
PR   20-APR-1999;   99WO-US08615.
PR   28-APR-1999;   99US-0131445.
PR   04-MAY-1999;   99US-0132371.
PR   14-MAY-1999;   99US-0134287.
PR   02-JUN-1999;   99WO-US12252.
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
PR   28-JUL-1999;   99US-0146222.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   13-SEP-1999;   99WO-US20944.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   05-OCT-1999;   99WO-US23089.
PR   29-OCT-1999;   99US-0162506.
PR   29-NOV-1999;   99WO-US28214.
PR   30-NOV-1999;   99WO-US28313.
PR   30-NOV-1999;   99WO-US28409.
PR   01-DEC-1999;   99WO-US28301.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   02-DEC-1999;   99WO-US28564.
PR   02-DEC-1999;   99WO-US28565.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30999.
PR   30-DEC-1999;   99WO-US31274.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00277.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Goddard A,  Gurney AL,  Hebert C,  Henzel W;
PI   Kabakoff RC,  Lu Y,  Pan J,  Pennica D,  Shelton DL,  Smith V;
PI   Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Yan M;
XX
DR   WPI; 2000-572271/53.
DR   N-PSDB; AAC58581.
XX
PT   Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT   immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT   arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
XX
PS   Claim 33; Fig 6; 309pp; English.
XX
CC   The present invention describes sixty four human PRO proteins which can
CC   be used in the treatment of immune related diseases. The human PRO
CC   proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC   treating and diagnosing immune related disorders. The disorders are
CC   selected from systemic lupus erythematosus, rheumatoid arthritis,
CC   osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC   systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC   syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC   anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC   immune-mediated renal disease, demyelinating diseases of the central
CC   and peripheral nervous systems, hepatobiliary diseases, inflammatory
CC   bowel disease, gluten-sensitive enteropathy and Whipple's disease,
CC   autoimmune or immune-mediated skin diseases, allergic diseases,
CC   immunological diseases of the lung, and transplantation associated
```

```
CC   diseases including graft rejection and graft-versus-host-disease.
CC   AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
CC   in the isolation of human PRO sequences. AAC58579 to AAC58642 and
CC   AAB33414 to AAB33477 represent human PRO polynucleotide and protein
CC   sequences given in the exemplification of the present invention.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 300;  DB 21;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-269;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 13
AAB03621
ID   AAB03621 standard; Protein; 300 AA.
XX
AC   AAB03621;
XX
DT   03-JAN-2001  (first entry)
XX
DE   Human Fas ligand inhibitor FLINT.
XX
KW   Human; Fas ligand inhibitor; FLINT; apoptosis; autoimmune disease;
KW   inflammation; infectious disease; ischaemia; Alzheimer's disease;
KW   Parkinson's disease; Crohn's disease; transplantation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1..29
FT                    /label= signal_peptide
FT   Protein          30..300
FT                    /label= mature_FLINT
FT   Domain           1..42
FT                    /label= domain_1
FT   Domain           43..85
FT                    /label= domain_2
FT   Domain           86..122
FT                    /label= domain_3
FT   Domain           123..165
FT                    /label= domain_4
XX
PN   WO200034782-A1.
XX
PD   15-JUN-2000.
XX
PF   07-DEC-1999;   99WO-US28696.
XX
PR   09-DEC-1998;   98US-0111575.
PR   09-DEC-1998;   98US-0111580.
PR   07-JAN-1999;   99US-0115069.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Rosteck PRJ,  Song HY,  Su EW;
XX
DR   WPI; 2000-431379/37.
DR   N-PSDB; AAA53208.
XX
PT   Novel monkey Fas ligand inhibitor polypeptides, useful for treating
PT   inflammatory or autoimmune disease such as rheumatoid arthritis,
PT   infectious diseases such as chronic hepatitis, and
PT   Ischaemia/Re-perfusion conditions -
XX
PS   Claim 19; Page 91-93; 101pp; English.
XX
CC   The present sequence is the protein sequence of the human Fas ligand
CC   inhibitor (FLINT). The FLINT protein is involved in cell-specific
CC   apoptosis, and can be used to treat inflammatory and autoimmune diseases
CC   such as rheumatoid arthritis, inflammatory bowel disease,
CC   graft-versus-host disease, diabetes, psoriasis and Graves' disease,
CC   infectious diseases such as HIV-induced lymphopenia, fulminant viral
CC   hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated
CC   ulceration, ischaemia and reperfusion conditions including acute
CC   myocardial infarction, acute coronary syndrome, congestive heart failure
CC   and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute lung
CC   injury and acute respiratory distress syndrome, Crohn's disease, brain
CC   trauma and injury, chronic glomerulonephritis, osteoporosis, aplastic
CC   anaemia, myelodysplasia, ulcerative colitis, Down's syndrome, and
CC   multiple sclerosis. In addition, the protein and its gene can be used to
CC   prevent apoptosis following organ transplantation.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 300;  DB 21;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-269;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 14
AAY97246
ID   AAY97246 standard; Protein; 300 AA.
XX
AC   AAY97246;
XX
DT   19-DEC-2000  (first entry)
XX
DE   M68 TNF receptor related protein.
XX
KW   M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;
KW   receptor; immune response; cell differentiation; ligand; cancer;
KW   bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
KW   Grave's disease; idiopathic myxodema; autoimmune diabetes;
KW   thrombotic thrombocytopenic purpura; multiple sclerosis;
KW   liver diseases; autoimmune gastritis; ulcerative colitis;
```

KW glomerulonephritis; pulmonary fibrosis; heart failure;
KW atherosclerosis; aplastic anaemia; myelodisplastic syndromes;
KW osteoporosis; Alzheimers disease; Parkinsons disease; stroke;
KW myocardial infarction; human.
XX
OS Homo sapiens.
XX
PN WO200046247-A1.
XX
PD 10-AUG-2000.
XX
PF 04-FEB-2000; 2000WO-US03037.
XX
PR 05-FEB-1999; 99US-0118902.
PR 20-DEC-1999; 99US-0172754.
XX
PA (MERI) MERCK & CO INC.
XX
PI Bai C;
XX
DR WPI; 2000-506066/45.
DR N-PSDB; AAA53800, AAA53801, AAA53802.
XX
PT Isolated human M68 nucleic acids and proteins which are part of the
PT tumor necrosis factor receptor (TNFR) family, useful for identifying
PT modulators that may be used to treat various diseases e.g. cancer,
PT osteoporosis, Alzheimer's disease
XX
PS Claim 1; Page 75-76; 80pp; English.
XX
CC The M68 protein is a member of a family of proteins which have
CC roles in immune responses, cell death, cell proliferation and
CC stimulation of cell differentiation. M68 lacks a transmembrane domain
CC and is a secreted factor suggesting that it functions as a natural
CC inhibitor for its ligand. The altered expression pattern of M68 in a
CC multitude of tissues suggests that M68 may play a role in cancer by
CC binding to its ligand and blocking apoptotic cell death induced by
CC such a ligand. This anti-apoptopic role of M68 suggests that
CC modulators of M68 will be useful in treatment of apoptosis-related
CC diseases such as various forms of cancer and various bone disorders.
CC M68 nucleic acids and proteins are therefore useful for treating
CC conditions involving atypical apoptosis and for identifying
CC modulators of M68. Modulators of M68 are useful for treatment of
CC cancer and other diseases associated with abnormal levels of
CC apoptosis including systemic lupus erythematosus, Hashimoto's
CC thyroiditis, Grave's disease, idiopathic myxodema, autoimmune
CC diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,
CC liver diseases, autoimmune gastritis, ulcerative colitis,
CC glomerulonephritis, pulmonary fibrosis, heart failure,
CC atherosclerosis, aplastic anaemia, myelodisplastic syndromes,
CC osteoporosis, Alzheimers disease, Parkinsons disease, stroke, and
CC myocardial infarction.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 300; DB 21; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.6e-269;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
```

RESULT 15
AAY90357
ID AAY90357 standard; Protein; 300 AA.
XX
AC AAY90357;
XX
DT 04-DEC-2000 (first entry)
XX
DE Human tumour necrosis factor receptor-6 alpha protein sequence.
XX
KW Human; Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;
KW ocular neovascularisation; solid tumour; malignancy; prostate cancer;
KW breast cancer; colon cancer; diabetic retinopathy; microbial infection;
KW pre-maturity macular degeneration; allergy; inflammation; tissue damage;
KW thyroid associated opthalmopathy; cell damage; parasitic infection;
KW bone disease; osteoporosis; atherosclerosis; cardiovascular disease;
KW neurodegenerative disorder; Alzheimer's disease; immune disorder;
KW graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma;
KW psoriasis; septic shock; ulcerative colitis; therapy.
XX
OS Homo sapiens.
XX
PN WO200052028-A1.
XX
PD 08-SEP-2000.
XX
PF 03-MAR-2000; 2000WO-US05686.
XX
PR 04-MAR-1999; 99US-0121774.
PR 12-MAR-1999; 99US-0124092.
PR 27-APR-1999; 99US-0131279.
PR 30-APR-1999; 99US-0131964.
PR 02-AUG-1999; 99US-0146371.
PR 01-DEC-1999; 99US-0168235.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Gentz RL, Ni J, Ebner R, Yu G, Ruben SM, Feng P;
XX
DR WPI; 2000-572174/53.
DR N-PSDB; AAA37772.
XX
PT Nucleic acids encoding human tumour necrosis factor receptor (TNFR)
PT proteins TNFR-6alpha and TNFR-6beta, useful for treating e.g.
PT Alzheimer's disease, osteoporosis and graft rejection -
XX
PS Claim 20; Fig 1; 332pp; English.
XX
CC This sequence represents the human tumour necrosis factor receptor 6
CC alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA
CC and protein sequences can be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate TNFR expression. The
CC nucleic acids, polypeptides, antibodies, agonists and antagonists against
CC them may be used for the treatment of a range of conditions such as
CC disorders associated with neovascularisation (especially ocular
CC neovascularisation) (such as solid tumours and malignancies (e.g.
CC prostate cancer, breast cancer and colon cancer), diabetic retinopathy
CC and pre-maturity macular degeneration), allergies, inflammation,
CC thyroid associated opthalmopathy tissue/cell damage, wounds, microbial
CC and parasitic infections, bone disease (e.g. osteoporosis),
CC atherosclerosis, pain, cardiovascular disease (e.g. stroke),
CC neurodegenerative disorders (e.g. Alzheimer's disease), immune
CC disorders (e.g. graft rejection), rheumatism, liver disease,
CC autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative
CC colitis.
XX

SQ Sequence 300 AA;

Query Match 100.0%; Score 300; DB 21; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.6e-269;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
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Search completed: July 16, 2003, 19:40:30
Job time : 39 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 16, 2003, 19:37:34 ; Search time 11 Seconds
(without alignments)
1131.173 Million cell updates/sec

Title: US-09-935-727-2
Perfect score: 300
Sequence: 1 MRALEGPGLSLLCLVLALPA.....RVARMPGLERSVRERFLPVH 300

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	300	100.0	300	1	TR6B_HUMAN	O95407 homo sapien
2	9	3.0	430	1	TRLT_HUMAN	Q969z4 homo sapien
3	9	3.0	430	1	TRLT_MACFA	Q9n092 macaca fasc
4	8	2.7	130	1	OREX_CANFA	Q9glf6 canis famil
5	8	2.7	130	1	OREX_MOUSE	O55241 mus musculu
6	8	2.7	130	1	OREX_RAT	O55232 rattus norv
7	8	2.7	131	1	OREX_HUMAN	O43612 homo sapien
8	8	2.7	131	1	OREX_PIG	O77668 sus scrofa
9	8	2.7	179	1	CAS2_RAT	P02667 rattus norv
10	8	2.7	184	1	CAS3_MOUSE	Q02862 mus musculu
11	8	2.7	494	1	ADRO_MOUSE	Q61578 mus musculu
12	8	2.7	530	1	YDEV_ECOLI	P77432 escherichia
13	8	2.7	626	1	GLMS_NOSS9	O68280 n glucosami
14	8	2.7	1172	1	TSP2_HUMAN	P35442 homo sapien
15	7	2.3	27	1	SECR_CANFA	P09910 canis famil
16	7	2.3	27	1	SECR_RABIT	P32647 oryctolagus
17	7	2.3	27	1	SECR_SHEEP	P31299 ovis aries
18	7	2.3	82	1	TX32_PHONI	O76201 phoneutria
19	7	2.3	113	1	IMM0_ECOLI	P33637 escherichia
20	7	2.3	113	1	IMM1_ECOLI	P02985 escherichia
21	7	2.3	113	1	IMM1_SHISO	P22558 shigella so
22	7	2.3	114	1	YOJ5_CAEEL	P34628 caenorhabdi
23	7	2.3	118	1	YNIF_AZOBR	P25316 azospirillu
24	7	2.3	121	1	SECR_HUMAN	P09683 homo sapien
25	7	2.3	131	1	SECR_PIG	P01279 sus scrofa
26	7	2.3	133	1	SECR_MOUSE	Q08535 mus musculu
27	7	2.3	134	1	SECR_RAT	P11384 rattus norv
28	7	2.3	145	1	TASM_BFDV	P13895 budgerigar
29	7	2.3	198	1	AMOS_DROME	Q9y0a7 drosophila
30	7	2.3	198	1	YH13_YEAST	P38896 saccharomyc
31	7	2.3	208	1	PYRF_PYRAB	Q9uz35 pyrococcus
32	7	2.3	208	1	PYRF_PYRHO	O58462 pyrococcus
33	7	2.3	211	1	PYRF_PYRFU	Q8ulu1 pyrococcus
34	7	2.3	214	1	YDH1_HSVS7	P25049 herpesvirus
35	7	2.3	230	1	RNS1_ARATH	P42813 arabidopsis
36	7	2.3	235	1	CAS2_PIG	P39036 sus scrofa
37	7	2.3	247	1	HXA4_HETFR	Q9ia22 heterodontu
38	7	2.3	270	1	HI7A_ARATH	P34047 arabidopsis
39	7	2.3	274	1	Y296_RICPR	Q9zdn1 rickettsia
40	7	2.3	277	1	Y495_MYCLE	P54579 mycobacteri
41	7	2.3	283	1	TR14_HUMAN	Q92956 homo sapien
42	7	2.3	315	1	SPY2_HUMAN	O43597 homo sapien
43	7	2.3	315	1	SPY2_MOUSE	Q9qxv8 mus musculu
44	7	2.3	323	1	TNR6_BOVIN	P51867 bos taurus
45	7	2.3	332	1	TNR6_PIG	O77736 sus scrofa

ALIGNMENTS

RESULT 1
TR6B_HUMAN
ID TR6B_HUMAN STANDARD; PRT; 300 AA.
AC O95407;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
DE receptor for Fas ligand) (Decoy receptor 3) (DcR3) (M68).
GN TNFRSF6B OR DCR3 OR TR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal lung;
RX MEDLINE=99087326; PubMed=9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Botstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
RC TISSUE=Prostate;
RX MEDLINE=99253915; PubMed=10318773;
RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20122600; PubMed=10655513;
RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M68/DcR3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Decoy receptor for the cytotoxic ligands TNFS14/LIGHT
CC and TNFSF6/FasL. Protects against apoptosis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.

```
CC       Detected in adult stomach, spinal cord, lymph node, trachea,
CC       spleen, colon and lung. Highly expressed in several primary tumors
CC       from colon, stomach, rectum, esophagus and in SW480 colon
CC       carcinoma cells.
CC   -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF104419; AAD03056.1; -.
DR   EMBL; AF134240; AAD29688.1; -.
DR   EMBL; AF217796; AAF35244.1; -.
DR   EMBL; AF217793; AAF33685.1; -.
DR   EMBL; AF217794; AAF33686.1; -.
DR   EMBL; AL121845; CAC03668.1; -.
DR   EMBL; BC017065; AAH17065.1; -.
DR   Genew; HGNC:11921; TNFRSF6B.
DR   MIM; 603361; -.
DR   HSSP; O14763; 1D0G.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 4.
DR   ProDom; PD000771; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     29
FT   CHAIN       30    300       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER 6B.
FT   REPEAT      31     70       TNFR-CYS 1.
FT   REPEAT      72    113       TNFR-CYS 2.
FT   REPEAT     115    150       TNFR-CYS 3.
FT   REPEAT     152    193       TNFR-CYS 4.
FT   DISULFID    49     62       BY SIMILARITY.
FT   DISULFID    52     70       BY SIMILARITY.
FT   DISULFID    73     88       BY SIMILARITY.
FT   DISULFID    91    105       BY SIMILARITY.
FT   DISULFID    95    113       BY SIMILARITY.
FT   DISULFID   115    126       BY SIMILARITY.
FT   DISULFID   132    150       BY SIMILARITY.
FT   DISULFID   153    168       BY SIMILARITY.
FT   DISULFID   174    193       BY SIMILARITY.
FT   CARBOHYD   173    173       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   300 AA;  32679 MW;  F90AEE33718449AF CRC64;

  Query Match           100.0%;  Score 300;  DB 1;  Length 300;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-273;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
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RESULT 2
TRLT_HUMAN
ID   TRLT_HUMAN     STANDARD;      PRT;   430 AA.
AC   Q969Z4; Q96JU1; Q9BUX7;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member TNFRSF19L precursor
DE   (Receptor expressed in lymphoid tissues).
GN   TNFRSF19L OR RELT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS.
RC   TISSUE=Lymphoma;
RX   MEDLINE=21213541; PubMed=11313261;
RA   Sica G.L., Zhu G., Tamada K., Liu D., Ni J., Chen L.;
RT   "RELT, a new member of the tumor necrosis factor receptor superfamily,
RT   is selectively expressed in hematopoietic tissues and activates
RT   transcription factor NF-kappaB.";
RL   Blood 97:2702-2707(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retinoblastoma;
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA   Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA   Ninomiya K., Iwayanagi T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon, and Eye;
RA   Strausberg R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 121-430 FROM N.A.
RC   TISSUE=Spleen;
RA   Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
RT   "The nucleotide sequence of a long cDNA clone isolated from human
RT   spleen.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Mediates activation of NF-kappa-B. May play a role in T-
CC       cell activation.
CC   -!- SUBUNIT: Associates with TRAF1.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -!- TISSUE SPECIFICITY: Highest levels are in spleen, lymph node,
CC       thymus, peripheral blood leukocytes, bone marrow and fetal liver.
CC       Very low levels in skeletal muscle, testis and colon. Not detected
CC       in brain, kidney and pancreas.
CC   -!- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
CC   -!- CAUTION: Ref.4 sequence differs from that shown due to several
CC       frameshifts.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF319553; AAK77356.1; -.
DR   EMBL; AK027899; BAB55441.1; -.
DR   EMBL; BC001812; AAH01812.1; -.
DR   EMBL; BC017279; AAH17279.1; -.
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DR   EMBL; AK074128; BAB84954.1; ALT_FRAME.
DR   Genew; HGNC:13764; TNFRSF19L.
DR   PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR   PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW   Receptor; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL       1     26
FT   CHAIN       27    430       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER TNFRSF19L.
FT   DOMAIN      27    162       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   163    183       POTENTIAL.
FT   DOMAIN     184    430       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      50     90       TNFR-CYS.
FT   DISULFID    51     65       BY SIMILARITY.
FT   DISULFID    71     90       BY SIMILARITY.
FT   CARBOHYD   149    149       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   122    122       D -> S (IN REF. 4).
FT   CONFLICT   187    187       K -> E (IN REF. 2).
FT   CONFLICT   273    273       H -> R (IN REF. 2).
FT   CONFLICT   379    380       DL -> TR (IN REF. 3; AAH01812).
SQ   SEQUENCE   430 AA;  46092 MW;  4A5AB9AE32D36101 CRC64;

  Query Match             3.0%;  Score 9;  DB 1;  Length 430;
  Best Local Similarity   100.0%;  Pred. No. 1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        152 PCPPGTFSA 160
              |||||||||
Db         50 PCPPGTFSA 58


RESULT 3
TRLT_MACFA
ID   TRLT_MACFA     STANDARD;      PRT;   430 AA.
AC   Q9N092;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member TNFRSF19L precursor
DE   (Receptor expressed in lymphoid tissues).
GN   TNFRSF19L OR RELT.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21458551; PubMed=11574149;
RA   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y.,
RA   Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K., Kususda J.;
RT   "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
RT   chromosomes.";
RL   Gene 275:31-37(2001).
CC   -!- FUNCTION: Mediates activation of NF-kappa-B (By similarity). May
CC       play a role in T-cell activation.
CC   -!- SUBUNIT: Associates with TRAF1 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC   -!- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB046039; BAB01621.1; -.
DR   InterPro; IPR001368; TNFR_c6.
DR   PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR   PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
DR   SMART; SM00208; TNFR; 1.
KW   Receptor; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL       1     26       BY SIMILARITY.
FT   CHAIN       27    430       TUMOR NECROSIS FACTOR RECEPTOR
FT                               SUPERFAMILY MEMBER TNFRSF19L.
FT   DOMAIN      27    162       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   163    183       POTENTIAL.
FT   DOMAIN     184    430       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      50     90       TNFR-CYS.
FT   DISULFID    51     65       BY SIMILARITY.
FT   DISULFID    71     90       BY SIMILARITY.
FT   CARBOHYD   149    149       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   430 AA;  45850 MW;  BA8DE92593E1E859 CRC64;

  Query Match             3.0%;  Score 9;  DB 1;  Length 430;
  Best Local Similarity   100.0%;  Pred. No. 1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        152 PCPPGTFSA 160
              |||||||||
Db         50 PCPPGTFSA 58


RESULT 4
OREX_CANFA
ID   OREX_CANFA     STANDARD;      PRT;   130 AA.
AC   Q9GLF6;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Orexin precursor (Hypocretin) (Hcrt) [Contains: Orexin-A (Hypocretin-
DE   1) (Hcrt1); Orexin-B (Hypocretin-2) (Hcrt2)].
GN   HCRT OR OX OR PPOX.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A., AND VARIANT THR-30.
RX   MEDLINE=21180003; PubMed=11282968;
RA   Hungs M., Fan J., Lin L., Lin X., Maki R.A., Mignot E.;
RT   "Identification and functional analysis of mutations in the hypocretin
RT   (orexin) genes of narcoleptic canines.";
RL   Genome Res. 11:531-539(2001).
RN   [2]
RP   REVIEW.
RX   MEDLINE=21237974; PubMed=11340621;
RA   Hungs M., Mignot E.;
RT   "Hypocretin/orexin, sleep and narcolepsy.";
RL   Bioessays 23:397-408(2001).
RN   [3]
RP   REVIEW.
RX   MEDLINE=21178476; PubMed=11283317;
RA   Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
RT   "To eat or to sleep? Orexin in the regulation of feeding and
RT   wakefulness.";
RL   Annu. Rev. Neurosci. 24:429-458(2001).
CC   -!- FUNCTION: Neuropeptides that play a significant role in the
CC       regulation of food intake and sleep-wakefulness, possibly by
CC       coordinating the complex behavioral and physiologic responses of
CC       these complementary homeostatic functions. A broader role in the
CC       homeostatic regulation of energy metabolism, autonomic function,
CC       hormonal balance and the regulation of body fluids, is also
CC       suggested. Orexin-A binds to both OX1R and OX2R with a high
CC       affinity, whereas orexin-B binds only to OX2R with a similar high
CC       affinity.
CC   -!- SUBCELLULAR LOCATION: ASSOCIATED WITH PERIKARYAL ROUGH ENDOPLASMIC
CC       RETICULUM AS WELL AS CYTOPLASMIC LARGE GRANULAR VESICLES AT
CC       SYNAPSES (BY SIMILARITY).
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD
CC       THE DIFFERENT ACTIVE PEPTIDES.
CC   -!- SIMILARITY: BELONGS TO THE OREXIN FAMILY.
CC   -!- DATABASE: NAME=Protein Spotlight;
CC       NOTE=Issue 15 of October 2001;
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CC       WWW="http://www.expasy.org/spotlight/articles/sptlt015.html".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF285110; AAG13965.1; -.
DR   InterPro; IPR001704; Orexin.
DR   Pfam; PF02072; Orexin; 1.
DR   PRINTS; PR01091; OREXINPP.
KW   Neuropeptide; Cleavage on pair of basic residues; Signal; Amidation;
KW   Polymorphism.
FT   SIGNAL       1     32       BY SIMILARITY.
FT   PEPTIDE      33    65       OREXIN-A.
FT   PEPTIDE      69    96       OREXIN-B.
FT   PROPEP       97    130
FT   MOD_RES      33    33       PYRROLIDONE CARBOXYLIC ACID (BY
FT                               SIMILARITY).
FT   MOD_RES      65    65       AMIDATION (G-66 PROVIDE AMIDE GROUP) (BY
FT                               SIMILARITY).
FT   MOD_RES      96    96       AMIDATION (G-97 PROVIDE AMIDE GROUP) (BY
FT                               SIMILARITY).
FT   DISULFID     38    44       BY SIMILARITY.
FT   DISULFID     39    46       BY SIMILARITY.
FT   VARIANT      30    30       A -> T.
SQ   SEQUENCE   130 AA;  13328 MW;  2BF59D4C1E422DF3 CRC64;

  Query Match          2.7%;  Score 8;  DB 1;  Length 130;
  Best Local Similarity  100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        228 RLQRLLQA 235
              ||||||||
Db         78 RLQRLLQA 85


RESULT 5
OREX_MOUSE
ID   OREX_MOUSE     STANDARD;      PRT;   130 AA.
AC   O55241;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Orexin precursor (Hypocretin) (Hcrt) [Contains: Orexin-A (Hypocretin-
DE   1) (Hcrt1); Orexin-B (Hypocretin-2) (Hcrt2)].
GN   HCRT OR OX OR PPOX.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98150861; PubMed=9491897;
RA   Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,
RA   Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,
RA   Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,
RA   McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,
RA   Yanagisawa M.;
RT   "Orexins and orexin receptors: a family of hypothalamic neuropeptides
RT   and G protein-coupled receptors that regulate feeding behavior.";
RL   Cell 92:573-585(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=98081872; PubMed=9419374;
RA   de Lecea L., Kilduff T.S., Peyron C., Gao X.-B., Foye P.E.,
RA   Danielson P.E., Fukuhara C., Battenberg E.L.F., Gautvik V.T.,
RA   Bartlett F.S. II, Frankel W.N., van den Pol A.N., Bloom F.E.,
RA   Gautvik K.M., Sutcliffe J.G.;
RT   "The hypocretins: hypothalamus-specific peptides with neuroexcitatory
RT   activity.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:322-327(1998).
RN   [3]
RP   REVIEW.
RX   MEDLINE=21237974; PubMed=11340621;
RA   Hungs M., Mignot E.;
RT   "Hypocretin/orexin, sleep and narcolepsy.";
RL   Bioessays 23:397-408(2001).
RN   [4]
RP   REVIEW.
RX   MEDLINE=21178476; PubMed=11283317;
RA   Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
RT   "To eat or to sleep? Orexin in the regulation of feeding and
RT   wakefulness.";
RL   Annu. Rev. Neurosci. 24:429-458(2001).
CC   -!- FUNCTION: Neuropeptides that play a significant role in the
CC       regulation of food intake and sleep-wakefulness, possibly by
CC       coordinating the complex behavioral and physiologic responses of
CC       these complementary homeostatic functions. A broader role in the
CC       homeostatic regulation of energy metabolism, autonomic function,
CC       hormonal balance and the regulation of body fluids, is also
CC       suggested. Orexin-A binds to both OX1R and OX2R with a high
CC       affinity, whereas orexin-B binds only to OX2R with a similar high
CC       affinity.
CC   -!- SUBCELLULAR LOCATION: ASSOCIATED WITH PERIKARYAL ROUGH ENDOPLASMIC
CC       RETICULUM AS WELL AS CYTOPLASMIC LARGE GRANULAR VESICLES AT
CC       SYNAPSES (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: RESTRICTED TO NEURONAL CELL BODIES OF THE
CC       DORSAL AND LATERAL HYPOTHALAMUS.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD
CC       THE DIFFERENT ACTIVE PEPTIDES.
CC   -!- SIMILARITY: BELONGS TO THE OREXIN FAMILY.
CC   -!- DATABASE: NAME=Protein Spotlight;
CC       NOTE=Issue 15 of October 2001;
CC       WWW="http://www.expasy.org/spotlight/articles/sptlt015.html".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF041242; AAC40040.1; -.
DR   EMBL; AF019566; AAC02934.1; -.
DR   MGD; MGI:1202306; Hcrt.
DR   InterPro; IPR001704; Orexin.
DR   Pfam; PF02072; Orexin; 1.
DR   PRINTS; PR01091; OREXINPP.
KW   Neuropeptide; Cleavage on pair of basic residues; Signal; Amidation.
FT   SIGNAL       1     32       BY SIMILARITY.
FT   PEPTIDE      33    65       OREXIN-A.
FT   PEPTIDE      69    96       OREXIN-B.
FT   PROPEP       97    130
FT   MOD_RES      33    33       PYRROLIDONE CARBOXYLIC ACID (BY
FT                               SIMILARITY).
FT   MOD_RES      65    65       AMIDATION (G-66 PROVIDE AMIDE GROUP) (BY
FT                               SIMILARITY).
FT   MOD_RES      96    96       AMIDATION (G-97 PROVIDE AMIDE GROUP) (BY
FT                               SIMILARITY).
FT   DISULFID     38    44       BY SIMILARITY.
FT   DISULFID     39    46       BY SIMILARITY.
SQ   SEQUENCE   130 AA;  13503 MW;  D3C223F9EE835F1C CRC64;

  Query Match          2.7%;  Score 8;  DB 1;  Length 130;
  Best Local Similarity  100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        228 RLQRLLQA 235
              ||||||||
Db         78 RLQRLLQA 85
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RESULT 6
OREX_RAT
ID   OREX_RAT       STANDARD;      PRT;   130 AA.
AC   O55232;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Orexin precursor (Hypocretin) (Hcrt) [Contains: Orexin-A (Hypocretin-
DE   1) (Hcrt1); Orexin-B (Hypocretin-2) (Hcrt2)].
GN   HCRT OR OX OR PPOX.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 33-65 AND 69-96.
RC   TISSUE=Brain;
RX   MEDLINE=98150861; PubMed=9491897;
RA   Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,
RA   Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,
RA   Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,
RA   McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,
RA   Yanagisawa M.;
RT   "Orexins and orexin receptors: a family of hypothalamic neuropeptides
RT   and G protein-coupled receptors that regulate feeding behavior.";
RL   Cell 92:573-585(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=98081872; PubMed=9419374;
RA   de Lecea L., Kilduff T.S., Peyron C., Gao X.-B., Foye P.E.,
RA   Danielson P.E., Fukuhara C., Battenberg E.L.F., Gautvik V.T.,
RA   Bartlett F.S. II, Frankel W.N., van den Pol A.N., Bloom F.E.,
RA   Gautvik K.M., Sutcliffe J.G.;
RT   "The hypocretins: hypothalamus-specific peptides with neuroexcitatory
RT   activity.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:322-327(1998).
RN   [3]
RP   REVIEW.
RX   MEDLINE=21237974; PubMed=11340621;
RA   Hungs M., Mignot E.;
RT   "Hypocretin/orexin, sleep and narcolepsy.";
RL   Bioessays 23:397-408(2001).
RN   [4]
RP   REVIEW.
RX   MEDLINE=21178476; PubMed=11283317;
RA   Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
RT   "To eat or to sleep? Orexin in the regulation of feeding and
RT   wakefulness.";
RL   Annu. Rev. Neurosci. 24:429-458(2001).
CC   -!- FUNCTION: Neuropeptides that play a significant role in the
CC       regulation of food intake and sleep-wakefulness, possibly by
CC       coordinating the complex behavioral and physiologic responses of
CC       these complementary homeostatic functions. A broader role in the
CC       homeostatic regulation of energy metabolism, autonomic function,
CC       hormonal balance and the regulation of body fluids, is also
CC       suggested. A modulation effect on luteinizing hormone-releasing
CC       hormone (LHRH) secrettion also suggests a more minor contribution
CC       to the regulation of reproductive function. Orexin-A binds to both
CC       OX1R and OX2R with a high affinity, whereas orexin-B binds only to
CC       OX2R with a similar high affinity.
CC   -!- SUBCELLULAR LOCATION: ASSOCIATED WITH PERIKARYAL ROUGH ENDOPLASMIC
CC       RETICULUM AS WELL AS CYTOPLASMIC LARGE GRANULAR VESICLES AT
CC       SYNAPSES.
CC   -!- TISSUE SPECIFICITY: Produced by a small group of neurons
CC       restricted to the lateral and posterior hypothalamus and
CC       perifornical areas. Positive neurons project widely throughout the
CC       entire neuroaxis. Particularly abundant projections in the
CC       cerebral cortex, olfactory bulb, hippocampus, amygdala, septum,
CC       diagonal band of Broca, bed nucleus of the stria terminalis,
CC       thalamus, anterior and posterior hypothalamus, midbrain,
CC       brainstem, and spinal cord. Immunoreactivity reported in the
CC       enteric nervous system and pancreas. In small amount, also
CC       detected in the testis.
CC   -!- DEVELOPMENTAL STAGE: DETECTED AS EARLY AS EMBRYONIC DAY 18, BUT
CC       EXPRESSION INCREASED DRAMATICALLY AFTER THE THIRD POSTNATAL WEEK.
CC   -!- INDUCTION: By nutritional state, up-regulated by fasting, fluid
CC       deprivation and insulin-induced hypoglycemia. Orexin-A
CC       immunoreactivity varies diurnally and peaks during the dark
CC       phase, in the pons and the location of locus coeruleus.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD
CC       THE DIFFERENT ACTIVE PEPTIDES.
CC   -!- MASS SPECTROMETRY: MW=3558.7; MW_ERR=0.1; METHOD=MALDI;
CC       RANGE=33-65.
CC   -!- SIMILARITY: BELONGS TO THE OREXIN FAMILY.
CC   -!- DATABASE: NAME=Protein Spotlight;
CC       NOTE=Issue 15 of October 2001;
CC       WWW="http://www.expasy.org/spotlight/articles/sptlt015.html".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF041241; AAC40039.1; -.
DR   EMBL; AF019565; AAC02933.1; -.
DR   InterPro; IPR001704; Orexin.
DR   Pfam; PF02072; Orexin; 1.
DR   PRINTS; PR01091; OREXINPP.
KW   Neuropeptide; Cleavage on pair of basic residues; Signal; Amidation.
FT   SIGNAL        1     32
FT   PEPTIDE      33     65       OREXIN-A.
FT   PEPTIDE      69     96       OREXIN-B.
FT   PROPEP       97    130
FT   MOD_RES      33     33       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      65     65       AMIDATION (G-66 PROVIDE AMIDE GROUP).
FT   MOD_RES      96     96       AMIDATION (G-97 PROVIDE AMIDE GROUP).
FT   DISULFID     38     44
FT   DISULFID     39     46
SQ   SEQUENCE   130 AA;  13645 MW;  00CAB259EDF2A404 CRC64;

  Query Match             2.7%;  Score 8; DB 1;  Length 130;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        228 RLQRLLQA 235
              ||||||||
Db         78 RLQRLLQA 85


RESULT 7
OREX_HUMAN
ID   OREX_HUMAN     STANDARD;      PRT;   131 AA.
AC   O43612;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Orexin precursor (Hypocretin) (Hcrt) [Contains: Orexin-A (Hypocretin-
DE   1) (Hcrt1); Orexin-B (Hypocretin-2) (Hcrt2)].
GN   HCRT OR OX OR PPOX OR PPORX.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98150861; PubMed=9491897;
RA   Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,
RA   Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,
RA   Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,
RA   McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,
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RA   Yanagisawa M.;
RT   "Orexins and orexin receptors: a family of hypothalamic neuropeptides
RT   and G protein-coupled receptors that regulate feeding behavior.";
RL   Cell 92:573-585(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99292744; PubMed=10364220;
RA   Sakurai T., Moriguchi T., Furuya K., Kajiwara N., Nakamura T.,
RA   Yanagisawa M., Goto K.;
RT   "Structure and function of human prepro-orexin gene.";
RL   J. Biol. Chem. 274:17771-17776(1999).
RN   [3]
RP   STRUCTURE BY NMR OF 70-97.
RX   MEDLINE=20050594; PubMed=10583376;
RA   Lee J.-H., Bang E., Chae K.-J., Kim J.-Y., Lee D.W., Lee W.;
RT   "Solution structure of a new hypothalamic neuropeptide, human
RT   hypocretin-2/orexin-B.";
RL   Eur. J. Biochem. 266:831-839(1999).
RN   [4]
RP   REVIEW.
RX   MEDLINE=21237974; PubMed=11340621;
RA   Hungs M., Mignot E.;
RT   "Hypocretin/orexin, sleep and narcolepsy.";
RL   Bioessays 23:397-408(2001).
RN   [5]
RP   REVIEW.
RX   MEDLINE=21178476; PubMed=11283317;
RA   Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
RT   "To eat or to sleep? Orexin in the regulation of feeding and
RT   wakefulness.";
RL   Annu. Rev. Neurosci. 24:429-458(2001).
RN   [6]
RP   VARIANT EARLY-ONSET NARCOLEPSY ARG-16, AND MUTAGENESIS OF LEU-16.
RX   MEDLINE=20429525; PubMed=10973318;
RA   Peyron C., Faraco J., Rogers W., Ripley B., Overeem S., Charnay Y.,
RA   Nevsimalova S., Aldrich M., Reynolds D., Albin R., Li R., Hungs M.,
RA   Pedrazzoli M., Padigaru M., Kucherlapati M., Fan J., Maki R.,
RA   Lammers G.J., Bouras C., Kucherlapati R., Nishino S., Mignot E.;
RT   "A mutation in a case of early onset narcolepsy and a generalized
RT   absence of hypocretin peptides in human narcoleptic brains.";
RL   Nat. Med. 6:991-997(2000).
CC   -!- FUNCTION: Neuropeptides that play a significant role in the
CC       regulation of food intake and sleep-wakefulness, possibly by
CC       coordinating the complex behavioral and physiologic responses of
CC       these complementary homeostatic functions. A broader role in the
CC       homeostatic regulation of energy metabolism, autonomic function,
CC       hormonal balance and the regulation of body fluids, is also
CC       suggested. Orexin-A binds to both OX1R and OX2R with a high
CC       affinity, whereas orexin-B binds only to OX2R with a similar high
CC       affinity.
CC   -!- SUBCELLULAR LOCATION: ASSOCIATED WITH PERIKARYAL ROUGH ENDOPLASMIC
CC       RETICULUM AS WELL AS CYTOPLASMIC LARGE GRANULAR VESICLES AT
CC       SYNAPSES (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN SUBTHALAMIC NUCLEUS
CC       BUT UNDETECTABLE IN OTHER BRAIN REGIONS TESTED (HYPOTHALAMUS WAS
CC       NOT TESTED) AND IN HEART, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE,
CC       KIDNEY AND PANCREAS.
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD
CC       THE DIFFERENT ACTIVE PEPTIDES.
CC   -!- DISEASE: Defects in HCRT are a cause of narcolepsy, a neurological
CC       disabling sleep disorder, characterized by excessive daytime
CC       sleepiness, sleep fragmentation, symptoms of abnormal rapid-eye-
CC       movement (REM) sleep, such as cataplexy, hypnagogic
CC       hallucinations, and sleep paralysis. Cataplexy is a sudden loss of
CC       muscle tone triggered by emotions, which is the most valuable
CC       clinical feature used to diagnose narcolepsy. Human narcolepsy is
CC       associated with a deficient orexin system. Orexins are absent
CC       and/or greatly diminished in the brain and cerebrospinal fluid
CC       (CSF) of most narcoleptic patients. Human narcolepsy is primarily
CC       a sporadically occurring disorder but familial clustering has been
CC       observed.
CC   -!- SIMILARITY: BELONGS TO THE OREXIN FAMILY.
CC   -!- DATABASE: NAME=Protein Spotlight;
CC       NOTE=Issue 15 of October 2001;
CC       WWW="http://www.expasy.org/spotlight/articles/sptlt015.html".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF041240; AAC39600.1; -.
DR   EMBL; AF118885; AAD24459.1; -.
DR   PDB; 1CQ0; 12-JAN-00.
DR   Genew; HGNC:4847; HCRT.
DR   MIM; 602358; -.
DR   MIM; 161400; -.
DR   InterPro; IPR001704; Orexin.
DR   Pfam; PF02072; Orexin; 1.
DR   PRINTS; PR01091; OREXINPP.
KW   Neuropeptide; Cleavage on pair of basic residues; Signal; Amidation;
KW   Disease mutation; 3D-structure.
FT   SIGNAL       1     33       BY SIMILARITY.
FT   PEPTIDE      34    66       OREXIN-A.
FT   PEPTIDE      70    97       OREXIN-B.
FT   PROPEP       98    131
FT   MOD_RES      34    34       PYRROLIDONE CARBOXYLIC ACID (BY
FT                               SIMILARITY).
FT   MOD_RES      66    66       AMIDATION (G-67 PROVIDE AMIDE GROUP) (BY
FT                               SIMILARITY).
FT   MOD_RES      97    97       AMIDATION (G-98 PROVIDE AMIDE GROUP) (BY
FT                               SIMILARITY).
FT   DISULFID     39    45       BY SIMILARITY.
FT   DISULFID     40    47       BY SIMILARITY.
FT   VARIANT      16    16       L -> R (IN EARLY-ONSET NARCOLEPSY).
FT                               /FTId=VAR_011633.
FT   MUTAGEN      16    16       L->R: IMPAIRED TRAFFICKING AND
FT                               PROCESSING.
SQ   SEQUENCE   131 AA;  13363 MW;  139D9C33E39E4EF1 CRC64;

  Query Match              2.7%;  Score 8;  DB 1;  Length 131;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        228 RLQRLLQA 235
              ||||||||
Db         79 RLQRLLQA 86


RESULT 8
OREX_PIG
ID   OREX_PIG       STANDARD;      PRT;   131 AA.
AC   O77668; Q9TTA6;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Orexin precursor (Hypocretin) (Hcrt) [Contains: Orexin-A (Hypocretin-
DE   1) (Hcrt1); Orexin-B (Hypocretin-2) (Hcrt2)].
GN   HCRT OR OX OR PPOX.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A., AND SYNTHESIS OF OREXIN-B.
RC   TISSUE=Hypothalamus;
RX   MEDLINE=99275384; PubMed=10343916;
RA   Dyer C.J., Touchette K.J., Carroll J.A., Allee G.L., Matteri R.L.;
RT   "Cloning of porcine prepro-orexin cDNA and effects of an intramuscular
RT   injection of synthetic porcine orexin-B on feed intake in young
RT   pigs.";
RL   Domest. Anim. Endocrinol. 16:145-148(1999).
RN   [2]
```

```
RP   SEQUENCE OF 3-131 FROM N.A.
RA   Malek M., Marklund S., Rothschild M.F.;
RT   "Linkage and physical mapping of the porcine prepro-orexin gene.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Neuropeptides that play a significant role in the
CC       regulation of food intake and sleep-wakefulness, possibly by
CC       coordinating the complex behavioral and physiologic responses of
CC       these complementary homeostatic functions. A broader role in the
CC       homeostatic regulation of energy metabolism, autonomic function,
CC       hormonal balance and the regulation of body fluids, is also
CC       suggested. Orexin-A binds to both OX1R and OX2R with a high
CC       affinity, whereas orexin-B binds only to OX2R with a similar high
CC       affinity (By similarity).
CC   -!- SUBCELLULAR LOCATION: ASSOCIATED WITH PERIKARYAL ROUGH ENDOPLASMIC
CC       RETICULUM AS WELL AS CYTOPLASMIC LARGE GRANULAR VESICLES AT
CC       SYNAPSES (BY SIMILARITY).
CC   -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES AT PAIRED BASIC RESIDUES YIELD
CC       THE DIFFERENT ACTIVE PEPTIDES.
CC   -!- SIMILARITY: BELONGS TO THE OREXIN FAMILY.
CC   -!- DATABASE: NAME=Protein Spotlight;
CC       NOTE=Issue 15 of October 2001;
CC       WWW="http://www.expasy.org/spotlight/articles/sptlt015.html".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF075241; AAC26827.1; -.
DR   EMBL; AF169352; AAF24216.1; -.
DR   InterPro; IPR001704; Orexin.
DR   Pfam; PF02072; Orexin; 1.
DR   PRINTS; PR01091; OREXINPP.
KW   Neuropeptide; Cleavage on pair of basic residues; Signal; Amidation.
FT   SIGNAL       1     33       BY SIMILARITY.
FT   PEPTIDE      34    66       OREXIN-A.
FT   PEPTIDE      70    97       OREXIN-B.
FT   PROPEP       98    131
FT   MOD_RES      34    34       PYRROLIDONE CARBOXYLIC ACID (BY
FT                               SIMILARITY).
FT   MOD_RES      66    66       AMIDATION (G-67 PROVIDE AMIDE GROUP) (BY
FT                               SIMILARITY).
FT   MOD_RES      97    97       AMIDATION (G-98 PROVIDE AMIDE GROUP) (BY
FT                               SIMILARITY).
FT   DISULFID     39    45       BY SIMILARITY.
FT   DISULFID     40    47       BY SIMILARITY.
SQ   SEQUENCE   131 AA;  13457 MW;  665A74448429AB1F CRC64;

  Query Match             2.7%;  Score 8;  DB 1;  Length 131;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        228 RLQRLLQA 235
              ||||||||
Db         79 RLQRLLQA 86


RESULT 9
CAS2_RAT
ID   CAS2_RAT       STANDARD;      PRT;   179 AA.
AC   P02667;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Gamma casein precursor.
GN   CSNG.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83143278; PubMed=6298707;
RA   Hobbs A.A., Rosen J.M.;
RT   "Sequence of rat alpha- and gamma-casein mRNAs: evolutionary
RT   comparison of the calcium-dependent rat casein multigene family.";
RL   Nucleic Acids Res. 10:8079-8098(1982).
CC   -!- FUNCTION: IMPORTANT ROLE IN THE CAPACITY OF MILK TO TRANSPORT
CC       CALCIUM PHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: Extracellular.
CC   -!- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
CC   -!- SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00712; -; NOT_ANNOTATED_CDS.
DR   PIR; A03111; KGRT.
DR   InterPro; IPR001588; Casein.
DR   Pfam; PF00363; caseins; 1.
DR   PROSITE; PS00306; CASEIN_ALPHA_BETA; 1.
KW   Milk; Phosphorylation; Signal.
FT   SIGNAL       1     15
FT   CHAIN        16    179       GAMMA CASEIN.
FT   MOD_RES      24    24        PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      25    25        PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      52    52        PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      53    53        PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      54    54        PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      55    55        PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      56    56        PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      59    59        PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      60    60        PHOSPHORYLATION (POTENTIAL).
SQ   SEQUENCE   179 AA;  20277 MW;  91B3EB95229976FD CRC64;

  Query Match             2.7%;  Score 8;  DB 1;  Length 179;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        159 SASSSSSE 166
              ||||||||
Db         50 SASSSSSE 57


RESULT 10
CAS3_MOUSE
ID   CAS3_MOUSE     STANDARD;      PRT;   184 AA.
AC   Q02862;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Gamma casein precursor (PP22).
GN   CSNG.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=93320737; PubMed=7763793;
RA   Sasaki T., Sasaki M., Enami J.;
RT   "Mouse gamma-casein cDNA: PCR cloning and sequence analysis.";
RL   Zool. Sci. 10:65-72(1993).
CC   -!- FUNCTION: IMPORTANT ROLE IN THE CAPACITY OF MILK TO TRANSPORT
CC       CALCIUM PHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: Extracellular.
CC   -!- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
CC   -!- SIMILARITY: BELONGS TO THE ALPHA-CASEIN FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D10215; BAA01067.1; -.
DR   MGD; MGI:88542; Csng.
DR   InterPro; IPR001588; Casein.
DR   Pfam; PF00363; caseins; 1.
KW   Milk; Phosphorylation; Signal.
FT   SIGNAL        1     15
FT   CHAIN        16    184       GAMMA CASEIN.
FT   MOD_RES      23     23       PHOSPHORYLATION.
FT   MOD_RES      24     24       PHOSPHORYLATION.
FT   MOD_RES      25     25       PHOSPHORYLATION.
FT   MOD_RES      37     37       PHOSPHORYLATION.
FT   MOD_RES      53     53       PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      54     54       PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      55     55       PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      56     56       PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      57     57       PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      60     60       PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      61     61       PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      71     71       PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      88     88       PHOSPHORYLATION (POTENTIAL).
SQ   SEQUENCE   184 AA;  21100 MW;  AE6EC45FD3E24A32 CRC64;

  Query Match             2.7%;  Score 8;  DB 1;  Length 184;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        159 SASSSSSE 166
              ||||||||
Db         51 SASSSSSE 58


RESULT 11
ADRO_MOUSE
ID   ADRO_MOUSE     STANDARD;      PRT;   494 AA.
AC   Q61578;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   NADPH:adrenodoxin oxidoreductase, mitochondrial precursor
DE   (EC 1.18.1.2) (Adrenodoxin reductase) (AR) (Ferredoxin-NADP(+)
DE   reductase).
GN   FDXR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Kidney;
RX   MEDLINE=96085117; PubMed=7495857;
RA   Itoh S., Iemura O., Yamada E., Yoshimura T., Tsujikawa K., Kohama Y.,
RA   Mimura T.;
RT   "cDNA cloning of mouse ferredoxin reductase from kidney.";
RL   Biochim. Biophys. Acta 1264:159-162(1995).
CC   -!- FUNCTION: SERVES AS THE FIRST ELECTRON TRANSFER PROTEIN IN ALL THE
CC       MITOCHONDRIAL P450 SYSTEMS. INCLUDING CHOLESTEROL SIDE CHAIN
CC       CLEAVAGE IN ALL STEROIDOGENIC TISSUES, STEROID 11-BETA
CC       HYDROXYLATION IN THE ADRENAL CORTEX, 25-OH-VITAMIN D3-24
CC       HYDROXYLATION IN THE KIDNEY, AND STEROL C-27 HYDROXYLATION IN THE
CC       LIVER.
CC   -!- CATALYTIC ACTIVITY: Reduced adrenodoxin + NADP(+) = oxidized
CC       adrenodoxin + NADPH.
CC   -!- COFACTOR: FAD.
CC   -!- PATHWAY: CHOLESTEROL SIDE-CHAIN-CLEAVAGE SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN THE ADRENAL, TESTIS AND OVARY AND
CC       TO A LESSER EXTENT IN THE LIVER AND KIDNEY.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D49920; BAA08659.1; -.
DR   HSSP; P08165; 1E6E.
DR   MGD; MGI:104724; Fdxr.
DR   InterPro; IPR000759; Adrndx_reductase.
DR   PRINTS; PR00419; ADXRDTASE.
KW   Electron transport; Oxidoreductase; Flavoprotein; NADP; FAD;
KW   Mitochondrion; Transit peptide.
FT   TRANSIT       1     34       MITOCHONDRION (POTENTIAL).
FT   CHAIN        35    494       NADPH:ADRENODOXIN OXIDOREDUCTASE.
SQ   SEQUENCE   494 AA;  54202 MW;  4BD279DFC606A5C5 CRC64;

  Query Match             2.7%;  Score 8;  DB 1;  Length 494;
  Best Local Similarity   100.0%;  Pred. No. 10;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        258 RRRLTELL 265
              ||||||||
Db        276 RRRLTELL 283


RESULT 12
YDEV_ECOLI
ID   YDEV_ECOLI     STANDARD;      PRT;   530 AA.
AC   P77432; Q99894;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical sugar kinase ydeV.
GN   YDEV OR B1511.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE=97251357; PubMed=9097039;
RA   Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA   Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
RA   Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
RA   Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
RA   Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
RA   Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
RA   Yamamoto Y., Horiuchi T.;
RT   "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT   corresponding to the 28.0-40.1 min region on the linkage map.";
RL   DNA Res. 3:363-377(1996).
RN   [3]
RP   SEQUENCE OF 182-495 FROM N.A.
RX   MEDLINE=96243037; PubMed=8649811;
RA   Das R., Reddy E.P., Chatterjee D., Andrews D.W.;
```

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RT   "Identification of a novel Bcl-2 related gene, BRAG-1, in human
RT   glioma.";
RL   Oncogene 12:947-951(1996).
CC   -!- SIMILARITY: BELONGS TO THE FUCOKINASE / GLUCONOKINASE /
CC       GLYCEROKINASE / XYLULOKINASE FAMILY.
CC   -!- CAUTION: WAS THOUGHT BY REF.3 TO BE A HUMAN SEQUENCE AND WAS
CC       CALLED BY THEM BRAG1 (BRAIN-RELATED APOPTOSIS GENE) (BRAG-1)
CC       WITH A ROLE IN APOPTOSIS. THE DNA SEQUENCE OF THE REGION THEY
CC       SEQUENCED IS MORE THAN 99% IDENTICAL TO THAT OF THIS E.COLI
CC       GENE. FURTHERMORE THEY CLAIM 'EXTENSIVE SIMILARITY TO THE
CC       BCL-2 FAMILY OF GENES.' SUCH A SIMILARITY IS NOT SIGNIFICANT
CC       AND THIS PROTEIN IS MUCH MORE LIKELY TO BE A SUGAR KINASE.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE000248; AAC74584.1; -.
DR   EMBL; D90793; BAA15191.1; -.
DR   EMBL; D90794; BAA15198.1; -.
DR   EMBL; S82185; AAC17184.1; -.
DR   EcoGene; EG13804; ydeV.
DR   InterPro; IPR000577; FGGY_kin.
DR   Pfam; PF00370; FGGY; 1.
DR   Pfam; PF02782; FGGY_C; 1.
DR   PROSITE; PS00933; FGGY_KINASES_1; FALSE_NEG.
DR   PROSITE; PS00445; FGGY_KINASES_2; FALSE_NEG.
KW   Hypothetical protein; Transferase; Kinase; Complete proteome.
FT   CONFLICT    490    495       PDPEKH -> TRPGKA (IN REF. 2).
SQ   SEQUENCE   530 AA;  57544 MW;  CBC3B1E7C8982063 CRC64;

  Query Match             2.7%;  Score 8;  DB 1;  Length 530;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         41 AETGERLV 48
              ||||||||
Db        475 AETGERLV 482


RESULT 13
GLMS_NOSS9
ID   GLMS_NOSS9     STANDARD;      PRT;   626 AA.
AC   O68280;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
DE   (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-
DE   phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate
DE   amidotransferase) (Glucosamine-6-phosphate synthase).
GN   GLMS OR NODM.
OS   Nostoc sp. (strain PCC 9229).
OC   Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX   NCBI_TaxID=70817;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Viterbo A., Matveyev A., Rasmussen U., Bergman B.;
RT   "Characterization of a nodM homologous gene in the symbiotic
RT   cyanobacterium Nostoc PCC 9229.";
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CATALYZES THE FIRST STEP IN HEXOSAMINE METABOLISM,
CC       CONVERTING FRUCTOSE-6P INTO GLUCOSAMINE-6P USING GLUTAMINE AS A
CC       NITROGEN SOURCE (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-
CC       glutamate + D-glucosamine 6-phosphate.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SIS FAMILY.
CC       GFAT SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 1 TYPE-2 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF028734; AAC17973.1; -.
DR   HSSP; P17169; 1GDO.
DR   MEROPS; C44.971; -.
DR   InterPro; IPR000583; GATase_2.
DR   InterPro; IPR001347; SIS.
DR   Pfam; PF00310; GATase_2; 1.
DR   Pfam; PF01380; SIS; 2.
DR   TIGRFAMs; TIGR01135; glmS; 1.
DR   PROSITE; PS00443; GATASE_TYPE_II; 1.
KW   Transferase; Aminotransferase; Glutamine amidotransferase.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   ACT_SITE      1      1       GATASE (BY SIMILARITY).
FT   ACT_SITE    621    621       ISOMERIZATION FRU-6P (BY SIMILARITY).
FT   DOMAIN        1    187       GLUTAMINE AMIDOTRANSFERASE.
SQ   SEQUENCE   626 AA;  68638 MW;  415FCF5046F2F1D3 CRC64;

  Query Match             2.7%;  Score 8;  DB 1;  Length 626;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        158 FSASSSSS 165
              ||||||||
Db        138 FSASSSSS 145


RESULT 14
TSP2_HUMAN
ID   TSP2_HUMAN     STANDARD;      PRT;  1172 AA.
AC   P35442;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Thrombospondin 2 precursor.
GN   THBS2 OR TSP2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94010892; PubMed=8406456;
RA   Labell T.L., Byers P.H.;
RT   "Sequence and characterization of the complete human thrombospondin 2
RT   cDNA: potential regulatory role for the 3' untranslated region.";
RL   Genomics 17:225-229(1993).
RN   [2]
RP   SEQUENCE OF 560-1172 FROM N.A.
RC   TISSUE=Fibroblast;
RX   MEDLINE=92217961; PubMed=1559694;
RA   Labell T.L., McGookey Milewicz D.J., Disteche C.M., Byers P.H.;
RT   "Thrombospondin II: partial cDNA sequence, chromosome location, and
RT   expression of a second member of the thrombospondin gene family in
RT   humans.";
RL   Genomics 12:421-429(1992).
CC   -!- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND
CC       CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN,
CC       LAMININ AND TYPE V COLLAGEN.
CC   -!- SUBUNIT: HOMOTRIMER; DISULFIDE-LINKED.
CC   -!- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
CC   -!- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
CC   -!- SIMILARITY: CONTAINS 7 TSP TYPE-3 DOMAINS.
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CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L12350; AAA03703.1; -.
DR   EMBL; M81339; -; NOT_ANNOTATED_CDS.
DR   PIR; A42173; A42173.
DR   HSSP; P00740; 1EDM.
DR   Genew; HGNC:11786; THBS2.
DR   MIM; 188061; -.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR001791; Laminin_G.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR003129; TSPN.
DR   InterPro; IPR001007; VWF_C.
DR   InterPro; IPR003367; tsp_3.
DR   Pfam; PF00008; EGF; 2.
DR   Pfam; PF00090; tsp_1; 3.
DR   Pfam; PF00093; vwc; 1.
DR   Pfam; PF02210; TSPN; 1.
DR   Pfam; PF02412; tsp_3; 9.
DR   SMART; SM00181; EGF; 3.
DR   SMART; SM00209; TSP1; 3.
DR   SMART; SM00210; TSPN; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS00022; EGF_1; FALSE_NEG.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS50092; TSP1; 3.
DR   PROSITE; PS01208; VWFC; 1.
KW   Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
KW   EGF-like domain; Signal.
FT   SIGNAL       1     18       POTENTIAL.
FT   CHAIN       19   1172       THROMBOSPONDIN 2.
FT   DOMAIN      19    232       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN     318    375       VWFC.
FT   DOMAIN     381    432       TSP TYPE-1 1.
FT   DOMAIN     437    493       TSP TYPE-1 2.
FT   DOMAIN     494    548       TSP TYPE-1 3.
FT   DOMAIN     549    589       EGF-LIKE 1.
FT   DOMAIN     590    647       EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN     648    692       EGF-LIKE 3.
FT   DOMAIN     725    760       TSP TYPE-3 1.
FT   DOMAIN     761    783       TSP TYPE-3 2.
FT   DOMAIN     784    819       TSP TYPE-3 3.
FT   DOMAIN     820    842       TSP TYPE-3 4.
FT   DOMAIN     843    880       TSP TYPE-3 5.
FT   DOMAIN     881    916       TSP TYPE-3 6.
FT   DOMAIN     917    952       TSP TYPE-3 7.
FT   DOMAIN     953   1172       C-TERMINAL.
FT   SITE       928    930       CELL ATTACHMENT SITE (POTENTIAL).
FT   DISULFID   266    266       INTERCHAIN (PROBABLE).
FT   DISULFID   270    270       INTERCHAIN (PROBABLE).
FT   DISULFID   553    564       BY SIMILARITY.
FT   DISULFID   558    574       BY SIMILARITY.
FT   DISULFID   577    588       BY SIMILARITY.
FT   DISULFID   594    610       BY SIMILARITY.
FT   DISULFID   601    619       BY SIMILARITY.
FT   DISULFID   622    646       BY SIMILARITY.
FT   DISULFID   652    665       BY SIMILARITY.
FT   DISULFID   659    678       BY SIMILARITY.
FT   DISULFID   680    691       BY SIMILARITY.
FT   CARBOHYD   151    151       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   316    316       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   330    330       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   457    457       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   584    584       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   710    710       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD  1069   1069       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   1172 AA;  129955 MW;  2AC7BB230E44C6F5 CRC64;

  Query Match             2.7%;  Score 8;  DB 1;  Length 1172;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 ALEGPGLS 10
              ||||||||
Db        102 ALEGPGLS 109


RESULT 15
SECR_CANFA
ID   SECR_CANFA     STANDARD;      PRT;    27 AA.
AC   P09910;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Secretin.
GN   SCT.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Intestine;
RX   MEDLINE=87314204; PubMed=3626755;
RA   Shinomura Y., Eng J., Yalow R.S.;
RT   "Dog secretin: sequence and biologic activity.";
RL   Life Sci. 41:1243-1248(1987).
CC   -!- FUNCTION: STIMULATES FORMATION OF NAHCO(3)-RICH PANCREATIC JUICE
CC       AND SECRETION OF NAHCO(3)-RICH BILE AND INHIBITS HCL PRODUCTION
CC       BY THE STOMACH.
CC   -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR   PIR; A27267; A27267.
DR   InterPro; IPR000532; Glucagon.
DR   Pfam; PF00123; hormone2; 1.
DR   PRINTS; PR00275; GLUCAGON.
DR   SMART; SM00070; GLUCA; 1.
DR   PROSITE; PS00260; GLUCAGON; 1.
KW   Glucagon family; Hormone; Amidation.
FT   MOD_RES      27     27       AMIDATION.
SQ   SEQUENCE   27 AA;  3070 MW;  2D4015814F955B78 CRC64;

  Query Match             2.3%;  Score 7;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        228 RLQRLLQ 234
              |||||||
Db         18 RLQRLLQ 24


Search completed: July 16, 2003, 19:41:18
Job time : 12 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 16, 2003, 19:39:04 ; Search time 33 Seconds
(without alignments)
1873.156 Million cell updates/sec

Title: US-09-935-727-2
Perfect score: 300
Sequence: 1 MRALEGPGLSLLCLVLALPA...:.....RVARMPGLERSVRERFLPVH 300

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10	3.3	343	5	Q95Q03	Q95q03 caenorhabdi
2	9	3.0	327	16	Q9I443	Q9i443 pseudomonas
3	9	3.0	561	10	Q9SH82	Q9sh82 arabidopsis
4	8	2.7	54	12	O89888	O89888 budgerigar
5	8	2.7	54	12	O89889	O89889 budgerigar
6	8	2.7	54	12	O89890	O89890 budgerigar
7	8	2.7	54	12	O89891	O89891 budgerigar
8	8	2.7	54	12	O89892	O89892 budgerigar
9	8	2.7	54	12	O89893	O89893 budgerigar
10	8	2.7	54	12	O89894	O89894 budgerigar
11	8	2.7	54	12	O89895	O89895 budgerigar
12	8	2.7	54	12	O89897	O89897 budgerigar
13	8	2.7	54	12	O89898	O89898 budgerigar
14	8	2.7	54	12	O89899	O89899 budgerigar
15	8	2.7	54	12	O89900	O89900 budgerigar
16	8	2.7	54	12	O89901	O89901 budgerigar
17	8	2.7	54	12	O89902	O89902 budgerigar
18	8	2.7	54	12	O89903	O89903 budgerigar
19	8	2.7	54	12	O89904	O89904 budgerigar
20	8	2.7	54	12	O89896	O89896 budgerigar
21	8	2.7	66	6	Q95L34	Q95l34 ovis aries
22	8	2.7	71	2	Q93M44	Q93m44 bordetella
23	8	2.7	145	12	Q9IBL0	Q9ibl0 budgerigar
24	8	2.7	145	12	Q9WG04	Q9wg04 budgerigar
25	8	2.7	181	10	O65446	O65446 arabidopsis
26	8	2.7	191	16	Q8X6G4	Q8x6g4 escherichia
27	8	2.7	206	2	Q9X6H9	Q9x6h9 streptococc
28	8	2.7	241	10	O49719	O49719 arabidopsis
29	8	2.7	269	4	Q9GZZ7	Q9gzz7 homo sapien
30	8	2.7	297	16	Q8ZCZ7	Q8zcz7 yersinia pe
31	8	2.7	299	4	Q9H192	Q9h192 homo sapien
32	8	2.7	308	11	Q923G5	Q923g5 rattus norv
33	8	2.7	308	11	Q91WU6	Q91wu6 mus musculu
34	8	2.7	341	5	Q9XXL8	Q9xxl8 caenorhabdi
35	8	2.7	364	17	Q8TWA8	Q8twa8 methanopyru
36	8	2.7	440	2	Q9JP96	Q9jp96 rhodocyclus
37	8	2.7	477	4	Q9Y577	Q9y577 homo sapien
38	8	2.7	493	4	Q96DP2	Q96dp2 homo sapien
39	8	2.7	494	16	Q8Z5S5	Q8z5s5 salmonella
40	8	2.7	504	5	Q9V4K7	Q9v4k7 drosophila
41	8	2.7	530	16	Q8XAY5	Q8xay5 escherichia
42	8	2.7	531	10	Q9STZ3	Q9stz3 arabidopsis
43	8	2.7	531	10	Q42582	Q42582 arabidopsis
44	8	2.7	587	12	Q9WG03	Q9wg03 budgerigar
45	8	2.7	599	12	Q9IBL1	Q9ibl1 budgerigar

ALIGNMENTS

RESULT 1
Q95Q03
ID Q95Q03 PRELIMINARY; PRT; 343 AA.
AC Q95Q03;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Y66D12A.12 protein.
GN Y66D12A.12.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Sulston J.E.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AL161712; CAC70134.1; -.
DR InterPro; IPR000822; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 2.
DR SMART; SM00355; ZnF_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_2.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW DNA-binding; Zinc-finger.
SQ SEQUENCE 343 AA; 37946 MW; E91F42FB5E72A210 CRC64;

Query Match 3.3%; Score 10; DB 5; Length 343;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 157 TFSASSSSSE 166
||||||||||

```
Db        202 TFSASSSSSE 211


RESULT 2
Q9I443
ID   Q9I443      PRELIMINARY;      PRT;   327 AA.
AC   Q9I443;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   Probable transmembrane sensor.
GN   PA1301.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC   Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
RL   Nature 406:959-964(2000).
DR   EMBL; AE004559; AAG04690.1; -.
KW   Transmembrane; Complete proteome.
SQ   SEQUENCE   327 AA;  36641 MW;  F4DE4A731326F23E CRC64;

  Query Match             3.0%;  Score 9;  DB 16;  Length 327;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 LALPALLPV 24
              |||||||||
Db        304 LALPALLPV 312


RESULT 3
Q9SH82
ID   Q9SH82      PRELIMINARY;      PRT;   561 AA.
AC   Q9SH82;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative Na+-dependent inorganic phosphate cotransporter.
GN   AT2G38060.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA   Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA   Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA   Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA   Salzberg S.L., Fraser C.M., Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Lin X.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR   EMBL; AC007661; AAD32766.1; -.
DR   InterPro; IPR003662; sub_transporter.
DR   Pfam; PF00083; sugar_tr; 1.
KW   Transmembrane.
SQ   SEQUENCE   561 AA;  61232 MW;  EEFB0BF3127E7680 CRC64;

  Query Match             3.0%;  Score 9;  DB 10;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 4.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GPGLSLLCL 14
              |||||||||
Db        405 GPGLSLLCL 413


RESULT 4
O89888
ID   O89888      PRELIMINARY;      PRT;    54 AA.
AC   O89888;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Large T and small t antigens (Fragment).
OS   Budgerigar fledgling disease virus (BFDV).
OC   Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX   NCBI_TaxID=10625;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MCFL97;
RA   Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
RT   "Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF054402; AAC33626.1; -.
DR   InterPro; IPR001623; DnaJ_N.
DR   Pfam; PF00226; DnaJ; 1.
DR   SMART; SM00271; DnaJ; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
FT   NON_TER      54      54
SQ   SEQUENCE   54 AA;  6077 MW;  5AF094925DE8C997 CRC64;

  Query Match             2.7%;  Score 8;  DB 12;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        259 RRLTELLG 266
              ||||||||
Db          5 RRLTELLG 12


RESULT 5
O89889
ID   O89889      PRELIMINARY;      PRT;    54 AA.
AC   O89889;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Large T and small t antigens (Fragment).
OS   Budgerigar fledgling disease virus (BFDV).
OC   Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX   NCBI_TaxID=10625;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LBMI92;
RA   Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
RT   "Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF054403; AAC33627.1; -.
DR   InterPro; IPR001623; DnaJ_N.
DR   Pfam; PF00226; DnaJ; 1.
DR   SMART; SM00271; DnaJ; 1.
```

```
DR   PROSITE; PS50076; DNAJ_2; 1.
FT   NON_TER      54     54
SQ   SEQUENCE   54 AA;  6077 MW;  5AF094925DE8C997 CRC64;

  Query Match             2.7%;  Score 8;  DB 12;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        259 RRLTELLG 266
              ||||||||
Db          5 RRLTELLG 12


RESULT 6
O89890
ID   O89890      PRELIMINARY;      PRT;    54 AA.
AC   O89890;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Large T and small t antigens (Fragment).
OS   Budgerigar fledgling disease virus (BFDV).
OC   Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX   NCBI_TaxID=10625;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GCAZ92;
RA   Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
RT   "Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF054404; AAC33628.1; -.
DR   InterPro; IPR001623; DnaJ_N.
DR   Pfam; PF00226; DnaJ; 1.
DR   SMART; SM00271; DnaJ; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
FT   NON_TER      54     54
SQ   SEQUENCE   54 AA;  6077 MW;  5AF094925DE8C997 CRC64;

  Query Match             2.7%;  Score 8;  DB 12;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        259 RRLTELLG 266
              ||||||||
Db          5 RRLTELLG 12


RESULT 7
O89891
ID   O89891      PRELIMINARY;      PRT;    54 AA.
AC   O89891;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Large T and small t antigens (Fragment).
OS   Budgerigar fledgling disease virus (BFDV).
OC   Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX   NCBI_TaxID=10625;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ECTX91;
RA   Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
RT   "Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF054405; AAC33629.1; -.
DR   InterPro; IPR001623; DnaJ_N.
DR   Pfam; PF00226; DnaJ; 1.
DR   SMART; SM00271; DnaJ; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
FT   NON_TER      54     54
SQ   SEQUENCE   54 AA;  6077 MW;  5AF094925DE8C997 CRC64;

  Query Match             2.7%;  Score 8;  DB 12;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        259 RRLTELLG 266
              ||||||||
Db          5 RRLTELLG 12


RESULT 8
O89892
ID   O89892      PRELIMINARY;      PRT;    54 AA.
AC   O89892;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Large T and small t antigens (Fragment).
OS   Budgerigar fledgling disease virus (BFDV).
OC   Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX   NCBI_TaxID=10625;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LB85;
RA   Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
RT   "Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF054406; AAC33630.1; -.
DR   InterPro; IPR001623; DnaJ_N.
DR   Pfam; PF00226; DnaJ; 1.
DR   SMART; SM00271; DnaJ; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
FT   NON_TER      54     54
SQ   SEQUENCE   54 AA;  6077 MW;  5AF094925DE8C997 CRC64;

  Query Match             2.7%;  Score 8;  DB 12;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        259 RRLTELLG 266
              ||||||||
Db          5 RRLTELLG 12


RESULT 9
O89893
ID   O89893      PRELIMINARY;      PRT;    54 AA.
AC   O89893;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Large T and small t antigens (Fragment).
OS   Budgerigar fledgling disease virus (BFDV).
OC   Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX   NCBI_TaxID=10625;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=YCFL87;
RA   Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
RT   "Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF054407; AAC33631.1; -.
DR   InterPro; IPR001623; DnaJ_N.
DR   Pfam; PF00226; DnaJ; 1.
DR   SMART; SM00271; DnaJ; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
FT   NON_TER      54     54
SQ   SEQUENCE   54 AA;  6077 MW;  5AF094925DE8C997 CRC64;

  Query Match             2.7%;  Score 8;  DB 12;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        259 RRLTELLG 266
              ||||||||
```

```
Db          5 RRLTELLG 12


RESULT 10
O89894
ID   O89894      PRELIMINARY;      PRT;    54 AA.
AC   O89894;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Large T and small t antigens (Fragment).
OS   Budgerigar fledgling disease virus (BFDV).
OC   Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX   NCBI_TaxID=10625;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SCIL88;
RA   Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
RT   "Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF054408; AAC33632.1; -.
DR   InterPro; IPR001623; DnaJ_N.
DR   Pfam; PF00226; DnaJ; 1.
DR   SMART; SM00271; DnaJ; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
FT   NON_TER      54      54
SQ   SEQUENCE   54 AA;  6077 MW;  5AF094925DE8C997 CRC64;

  Query Match             2.7%;  Score 8;  DB 12;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        259 RRLTELLG 266
              ||||||||
Db          5 RRLTELLG 12


RESULT 11
O89895
ID   O89895      PRELIMINARY;      PRT;    54 AA.
AC   O89895;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Large T and small t antigens (Fragment).
OS   Budgerigar fledgling disease virus (BFDV).
OC   Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX   NCBI_TaxID=10625;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BDTX88;
RA   Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
RT   "Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF054409; AAC33633.1; -.
DR   InterPro; IPR001623; DnaJ_N.
DR   Pfam; PF00226; DnaJ; 1.
DR   SMART; SM00271; DnaJ; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
FT   NON_TER      54      54
SQ   SEQUENCE   54 AA;  6077 MW;  5AF094925DE8C997 CRC64;

  Query Match             2.7%;  Score 8;  DB 12;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        259 RRLTELLG 266
              ||||||||
Db          5 RRLTELLG 12


RESULT 12
O89897
ID   O89897      PRELIMINARY;      PRT;    54 AA.
AC   O89897;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Large T and small t antigens (Fragment).
OS   Budgerigar fledgling disease virus (BFDV).
OC   Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX   NCBI_TaxID=10625;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BDTX89;
RA   Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
RT   "Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF054411; AAC33635.1; -.
DR   InterPro; IPR001623; DnaJ_N.
DR   Pfam; PF00226; DnaJ; 1.
DR   SMART; SM00271; DnaJ; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
FT   NON_TER      54      54
SQ   SEQUENCE   54 AA;  6077 MW;  5AF094925DE8C997 CRC64;

  Query Match             2.7%;  Score 8;  DB 12;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        259 RRLTELLG 266
              ||||||||
Db          5 RRLTELLG 12


RESULT 13
O89898
ID   O89898      PRELIMINARY;      PRT;    54 AA.
AC   O89898;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Large T and small t antigens (Fragment).
OS   Budgerigar fledgling disease virus (BFDV).
OC   Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX   NCBI_TaxID=10625;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BDGA81-A;
RA   Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
RT   "Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF054412; AAC33636.1; -.
DR   InterPro; IPR001623; DnaJ_N.
DR   Pfam; PF00226; DnaJ; 1.
DR   SMART; SM00271; DnaJ; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
FT   NON_TER      54      54
SQ   SEQUENCE   54 AA;  6077 MW;  5AF094925DE8C997 CRC64;

  Query Match             2.7%;  Score 8;  DB 12;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        259 RRLTELLG 266
              ||||||||
Db          5 RRLTELLG 12


RESULT 14
O89899
ID   O89899      PRELIMINARY;      PRT;    54 AA.
AC   O89899;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
```

```
DE   Large T and small t antigens (Fragment).
OS   Budgerigar fledgling disease virus (BFDV).
OC   Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX   NCBI_TaxID=10625;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BDGA81-B;
RA   Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
RT   "Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF054413; AAC33637.1; -.
DR   InterPro; IPR001623; DnaJ_N.
DR   Pfam; PF00226; DnaJ; 1.
DR   SMART; SM00271; DnaJ; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
FT   NON_TER      54     54
SQ   SEQUENCE   54 AA;  6077 MW;  5AF094925DE8C997 CRC64;

  Query Match             2.7%;  Score 8;  DB 12;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        259 RRLTELLG 266
              ||||||||
Db          5 RRLTELLG 12


RESULT 15
O89900
ID   O89900      PRELIMINARY;      PRT;    54 AA.
AC   O89900;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Large T and small t antigens (Fragment).
OS   Budgerigar fledgling disease virus (BFDV).
OC   Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX   NCBI_TaxID=10625;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BCFL92;
RA   Phalen D.N., Wilson V.G., Gaskin J.M., Derr J.N., Graham D.L.;
RT   "Genetic Diversity in 20 Variants of the Avian Polyomavirus.";
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF054414; AAC33638.1; -.
DR   InterPro; IPR001623; DnaJ_N.
DR   Pfam; PF00226; DnaJ; 1.
DR   SMART; SM00271; DnaJ; 1.
DR   PROSITE; PS50076; DNAJ_2; 1.
FT   NON_TER      54     54
SQ   SEQUENCE   54 AA;  6077 MW;  5AF094925DE8C997 CRC64;

  Query Match             2.7%;  Score 8;  DB 12;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        259 RRLTELLG 266
              ||||||||
Db          5 RRLTELLG 12


Search completed: July 16, 2003, 19:41:59
Job time : 35 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 16, 2003, 19:25:33 ; Search time 38 Seconds
(without alignments)
1051.979 Million cell updates/sec

Title: US-09-935-727-2
Perfect score: 1634
Sequence: 1 MRALEGPGLSLLCLVLALPA.....RVARMPGLERSVRERFLPVH 300

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1634	100.0	300	19	AAW66102	Amino acid sequenc
2	1634	100.0	300	19	AAW63622	Human tumour necro
3	1634	100.0	300	20	AAY03099	Human lung TNF-rec
4	1634	100.0	300	20	AAY42182	Human FLINT #1 pro
5	1634	100.0	300	20	AAY17479	Mammalian tumour n
6	1634	100.0	300	20	AAY06817	Human DcR3 polypep
7	1634	100.0	300	20	AAW97749	Human tumour necro
8	1634	100.0	300	20	AAW95082	Orphan receptor (H
9	1634	100.0	300	21	AAB19335	A full length huma
10	1634	100.0	300	21	AAB28559	Human soluble TNF
11	1634	100.0	300	21	AAB24057	Human PRO212 prote
12	1634	100.0	300	21	AAB33416	Human PRO212 prote
13	1634	100.0	300	21	AAB03621	Human Fas ligand i
14	1634	100.0	300	21	AAY97246	M68 TNF receptor r
15	1634	100.0	300	21	AAY90357	Human tumour necro
16	1634	100.0	300	21	AAB24395	Human PRO212 prote
17	1634	100.0	300	21	AAY96596	Human FLINT. Homo
18	1634	100.0	300	22	AAE03568	Human native fas l
19	1634	100.0	300	22	AAB74466	Human FLINT native
20	1634	100.0	300	22	AAB71754	Human NTR3. Homo
21	1634	100.0	300	22	AAB48161	Human PRO212 polyp
22	1634	100.0	300	22	AAB50903	Human PRO212 prote
23	1634	100.0	300	23	AAE14579	Human native FLINT
24	1634	100.0	300	23	AAE20848	Human tumour necro
25	1634	100.0	341	22	AAG73740	Human colon cancer
26	1620	99.1	300	21	AAY77458	Human TNF receptor
27	1619	99.1	300	21	AAB19710	Human FAS ligand i
28	1619	99.1	300	21	AAY96597	Human FLINT. Homo
29	1619	99.1	300	22	AAE03570	Human fas ligand i
30	1619	99.1	300	22	AAB83950	Amino acid sequenc
31	1619	99.1	300	22	AAB68045	Amino acid sequenc
32	1619	99.1	300	22	AAB68048	Amino acid sequenc
33	1619	99.1	300	23	AAE14580	Human FLINT analog
34	1610	98.5	302	20	AAY42183	Human FLINT #2 pro
35	1532	93.8	326	23	ABP41980	Human ovarian anti
36	1509	92.4	300	21	AAB03623	Human Fas ligand i
37	1502	91.9	300	21	AAB03622	Monkey Fas ligand
38	1502	91.9	300	21	AAB03624	Human Fas ligand i
39	1491	91.2	271	20	AAY42184	Human mFLINT #1 pr
40	1491	91.2	271	21	AAB19334	A mature human FAS
41	1491	91.2	271	21	AAB19705	Human FAS ligand i
42	1491	91.2	271	21	AAY97247	M68 TNF receptor r
43	1491	91.2	271	21	AAY96598	Human mature FLINT
44	1491	91.2	271	22	AAE03567	Human mature fas l
45	1491	91.2	271	22	AAB68044	Amino acid sequenc

ALIGNMENTS

RESULT 1
AAW66102
ID AAW66102 standard; Protein; 300 AA.
XX
AC AAW66102;
XX
DT 02-DEC-1998 (first entry)
XX
DE Amino acid sequence of tumour necrosis related receptor (TR4).
XX
KW Human; tumour necrosis related receptor; TR4; agonist; antagonist;
KW inhibition; chronic; acute; inflammation; arthritis; septicaemia;
KW autoimmune disease; transplant rejection; stroke; cancer;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN EP861850-A1.
XX
PD 02-SEP-1998.
XX
PF 20-JAN-1998; 98EP-0300382.
XX
PR 04-FEB-1997; 97US-0794796.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Emery J, Tan KB, Truneh A, Young PR;
XX
DR WPI; 1998-508248/44.
DR N-PSDB; AAV07654.
XX
PT New DNA encoding tumour necrosis related receptor - used to treat

```
PT   and prevent e.g. inflammation, arthritis, septicaemia, autoimmune
PT   diseases, transplant rejection, infection, stroke, ischaemia, ARDS,
PT   restenosis, AIDS, bone disorders and cancer
XX
PS   Claim 1; Fig 1; 21pp; English.
XX
CC   This is the amino acid sequence of the human tumour necrosis related
CC   receptor (TR4), used in the method of the invention.  The TR4 protein
CC   or its agonist can be used to treat a subject in need of enhanced
CC   TR4 polypeptide activity.  The antagonist is used to inhibit TR4
CC   polypeptide activity.  The active agents can be used for the
CC   treatment and prevention of diseases such as chronic and acute
CC   inflammation, arthritis, septicaemia, autoimmune diseases, transplant
CC   rejection, stroke, cancer, Alzheimer's disease.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 19;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
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Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
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Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
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Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 2
AAW63622
ID   AAW63622 standard; Protein; 300 AA.
XX
AC   AAW63622;
XX
DT   26-OCT-1998  (first entry)
XX
DE   Human tumour necrosis factor receptor-6 alpha protein.
XX
KW   Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
KW   endothelial cells; keratinocytes; normal prostate; apoptosis;
KW   prostate tumour tissue.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..30
FT   Protein         31..300
FT                   /note= "TNFR-6 alpha"
FT   Region          31..282
FT                   /note= "Soluble extracellular domain"
XX
PN   WO9830694-A2.
XX
PD   16-JUL-1998.
XX
PF   13-JAN-1998;   98WO-US00153.
XX
PR   14-JAN-1997;   97US-0035496.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ebner R,  Feng P,  Gentz RL,  Ni J,  Ruben SM,  Yu G;
XX
DR   WPI; 1998-399142/34.
DR   N-PSDB; AAV39085.
XX
PT   Human tumour necrosis factor receptors 6-alpha and 6-beta - used in
PT   the diagnosis of immune system-related disorder(s)
XX
PS   Claim 20; Fig 1; 91pp; English.
XX
CC   The present sequence represents the human tumour necrosis factor
CC   receptor-6 alpha (TNFR-6 alpha) protein.  The invention also provides
CC   for the TNFR-6 beta protein (AAW63623).  TNFR-6 alpha and TNFR-6 beta
CC   are members of the tumour necrosis factor receptor (TNFR) family.  TNFRs
CC   are expressed in endothelial cells, keratinocytes, normal prostate and
CC   prostate tumour tissue.  For a number of disorders of these cells,
CC   particularly of the immune system, substantially altered (whether
CC   increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene
CC   expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta
CC   polypeptides, nucleic acids and antibodies are claimed to be useful in
CC   the diagnosis of such disorders.  Mutations of the TNFR-6 alpha and
CC   TNFR-6 beta genes can also be detected.  The TNFR polypeptides are
CC   also claimed to be useful for identifying ligands which may be useful
CC   in the treatment of apoptosis related disorders.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 19;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 3
AAY03099
ID   AAY03099 standard; Protein; 300 AA.
XX
AC   AAY03099;
XX
DT   09-DEC-1999  (first entry)
XX
DE   Human lung TNF-receptor protein.
XX
KW   Tumour necrosis factor; TNF; TNF receptor; human; lung; gene therapy;
KW   detection; immunoassay; diagnosis; disease; immune system; tumour;
KW   osteogenic system; cardiovascular system; central nervous system; asthma;
KW   peripheral nervous systems; transplant incompatibility; antitumor;
KW   rheumatoid arthritis; antiasthmatic; antiarthritic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
```

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FT   CDS             134..1036
FT                   /*tag=  a
FT                   /product= "TNF-receptor"
XX
PN   DE19809978-A1.
XX
PD   16-SEP-1999.
XX
PF   09-MAR-1998;   98DE-1009978.
XX
PR   09-MAR-1998;   98DE-1009978.
XX
PA   (BADI ) BASF AG.
XX
PI   Kroeger B;
XX
DR   WPI; 1999-519473/44.
DR   N-PSDB; AAZ09998.
XX
PT   New soluble member of tumor necrosis factor receptor family, useful for
PT   identification specific modulators and for treating disease e.g. tumors
PT    -
XX
PS   Claim 1; Page 8-9; 10pp; German.
XX
CC   This invention describes a novel tumour necrosis factor (TNF) receptor
CC   (I) isolated from human lung tissue. (I) is used: (i) to raise specific
CC   antibodies (Ab); (ii) to screen for specific (ant)agonists or ligands
CC   (A), potential therapeutic agents; and (iii) therapeutically (optionally
CC   expressed from a gene therapy vector) in conditions associated with a
CC   deficit of (I). Ab are used: (a) for qualitative or quantitative
CC   detection of (I) in standard immunoassays (for diagnosis of disease, or
CC   susceptibility, or for monitoring); and (b) as therapeutic inhibitors in
CC   cases where (I) is overexpressed. Nucleic acid (II) that encodes (I) is
CC   used: (A) for recombinant production of (I); (B) also its oligonucleotide
CC   fragments, in standard hybridization and/or amplification assays; (C) as
CC   source of antisense molecules or ribozymes; and (D) to produce transgenic
CC   animals (for studying (patho)physiology of (I)). Diseases possibly
CC   associated with under- or over-expression of (I) are those of the immune,
CC   osteogenic, cardiovascular and central or peripheral nervous systems,
CC   tumors, transplant incompatibility, asthma and rheumatoid arthritis. The
CC   products of the invention have antitumor, antiasthmatic and
CC   antiarthritic activity. This sequence represents the TNF-receptor of the
CC   invention.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 20;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
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Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
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Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
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Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
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Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300

RESULT 4
AAY42182
ID   AAY42182 standard; Protein; 300 AA.
XX
AC   AAY42182;
XX
DT   17-DEC-1999  (first entry)
XX
DE   Human FLINT #1 protein sequence.
XX
KW   Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
KW   apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW   sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW   reperfusion-associated injury; aplastic anaemia; differentiation;
KW   growth; myelodysplastic syndrome; pancytopenic condition;
KW   myocardial ischaemia.
XX
OS   Homo sapiens.
XX
PN   WO9950413-A2.
XX
PD   07-OCT-1999.
XX
PF   30-MAR-1999;   99WO-US06797.
XX
PR   30-MAR-1998;   98US-0079856.
PR   20-MAY-1998;   98US-0086074.
PR   09-SEP-1998;   98US-0099643.
PR   17-DEC-1998;   98US-0112577.
PR   18-DEC-1998;   98US-0112703.
PR   18-DEC-1998;   98US-0112933.
PR   22-DEC-1998;   98US-0113407.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Bumol TF,  Dou S,  Glasebrook AL,  Gould KE,  Hale JE,  Heuer JG;
PI   Hui KY,  Kharitonenkov A,  Mizrahi J,  Na S,  Noblitt TW,  Reidy CA;
PI   Song HY,  Wang J,  Wu X,  Zuckerman SH;
XX
DR   WPI; 1999-591319/50.
DR   N-PSDB; AAZ25375.
XX
PT   Use of mature FLINT for treating acute liver failure, inflammation,
PT   cancer, and diabetes  - by prevention of FasL-Fas mediated apoptotic
PT   and proinflammatory activity
XX
PS   Claim 30; Fig 1; 99pp; English.
XX
CC   The present invention describes therapeutic applications of mature FLINT
CC   (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
CC   (mFLINT), which is a member of the tumour necrosis factor receptor
CC   superfamily, is used for treating acute liver failure, inflammation of
CC   the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
CC   with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
CC   injury or disorder such as hypercoagulation (including use with
CC   thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
CC   or disorder, Type I diabetes, cancer, cell damage or damage to an
CC   innocent bystander tissue that is induced by a chemotherapeutic agent or
CC   therapeutic irradiation, treating haematopoietic progenitor cells that
CC   have been exposed to therapeutic radiation or chemotherapy, aplastic
CC   anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
CC   also used for promoting the growth or differentiation of a haematopoietic
CC   progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
CC   resulting from abnormal myocardial ischaemia. The present sequence
CC   represents human FLINT.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 20;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
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Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

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Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
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Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
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Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
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Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
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RESULT 5
AAY17479
ID AAY17479 standard; Protein; 300 AA.
XX
AC AAY17479;
XX
DT 02-AUG-1999 (first entry)
XX
DE Mammalian tumour necrosis factor receptor OPG-2.
XX
KW Tumour necrosis factor receptor; TNF receptor; OPG-2; Paget's disease;
KW osteopenic disorder; osteoclast activity; primary osteoporosis;
KW hyperglycaemia; osteolytic metastasis; immune response; cancer.
XX
OS Mammalia.
XX
PN WO9926977-A1.
XX
PD 03-JUN-1999.
XX
PF 24-NOV-1998; 98WO-US25065.
XX
PR 17-FEB-1998; 98US-0074896.
PR 24-NOV-1997; 97US-0066446.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Tschopp J;
XX
DR WPI; 1999-347693/29.
DR N-PSDB; AAX76052.
XX
PT New tumour necrosis factor family receptor OPG-2
XX
PS Claim 1; Page 18; 22pp; English.
XX
CC The present sequence represents a mammalian tumour necrosis factor
CC receptor, designated OPG-2. OPG-2, is a member of the tumour necrosis
CC factor receptor family, and can be used: (i) to raise specific
CC antibodies (Ab), (ii) to treat osteopenic disorders associated with
CC excessive osteoclast activity, e.g. primary osteoporosis, Paget's
CC disease, hyperglycaemia of malignancy, or osteolytic metastases; (iii)
CC for affinity purification of cognate ligands, and (iv) to screen for
CC ligands (antagonists or agonists). Ab, or other OPG-2 blocking agents
CC such as soluble forms of the protein, are used to prevent, or reduce
CC severity of, an immune response, and for treating cancer. They can also
CC be used in diagnostic assays. The nucleic acid sequence encoding OPG-2
CC can be used as a probe to isolate related sequences from other species.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 20; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.4e-121;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
```

RESULT 6
AAY06817
ID AAY06817 standard; Protein; 300 AA.
XX
AC AAY06817;
XX
DT 24-JUN-1999 (first entry)
XX
DE Human DcR3 polypeptide.
XX
KW DcR3 polypeptide; tumour necrosis factor receptor; TNFR; Fas ligand;
KW apoptosis; T cell mediated immune response; allergy; asthma; cancer;
KW rheumatoid arthritis; Crohn's disease; guest vs. host disease; human;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO9914330-A1.
XX
PD 25-MAR-1999.
XX
PF 18-SEP-1998; 98WO-US19661.
XX
PR 30-JUL-1998; 98US-0094640.
PR 18-SEP-1997; 97US-0059288.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Botstein D, Dodge KH, Goddard A, Gurney AL;
PI Kim KJ, Lawrence DA, Pitti R, Roy MA, Tumas DB;
PI Wood WI;
XX
DR WPI; 1999-244032/20.
DR N-PSDB; AAX32744.
XX
PT DcR3 polypeptide related to tumor necrosis factor receptor
XX
PS Claim 5; Fig 1; 88pp; English.
XX
CC This represents a human DcR3 polypeptide, a homologue of tumour necrosis
CC factor receptor (TNFR) polypeptide. Host cells containing a vector
CC comprising the DcR3 nucleic acid can be used for the recombinant
CC expression of the protein. DcR3 binds to Fas ligand, so it (or its
CC chimeras) are useful for modulating apoptosis in mammalian cells, also
CC other Fas-ligand induced activities, particularly to inhibit T cell
CC mediated immune responses, e.g. in treatment of allergy, asthma,
CC rheumatoid arthritis, Crohn's disease, guest vs. host disease etc. DcR3
CC may also be used to identify specific binding proteins, potential
CC inhibitors. Antibodies against DcR3 are used to treat cancer,
CC specifically of the lung and colon, also in diagnosis and for affinity
CC purification of the protein. Detecting mutations in the gene for DcR3 is

```
CC   also used to diagnose cancer, or predisposition to it. DcR3 nucleic acid
CC   is useful as hybridization probe to detect genomic or related sequences;
CC   for chromosome and gene mapping; as source of antisense sequences; for
CC   expression of recombinant DcR3 and to generate transgenic animals (for
CC   development and screening of therapeutic agents), also for in vivo or
CC   ex vivo gene therapy.
XX
SQ   Sequence   300 AA;

  Query Match            100.0%;  Score 1634;  DB 20;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 7
AAW97749
ID   AAW97749 standard; Protein; 300 AA.
XX
AC   AAW97749;
XX
DT   21-MAY-1999  (first entry)
XX
DE   Human tumour necrosis factor receptor ZTNFR-5.
XX
KW   ZTNFR-5; tumour necrosis factor receptor; TNFR; human;
KW   cell maturation; bone cell regulation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..23
FT                   /note= "signal peptide"
FT   Protein         24..300
FT                   /note= "mature protein"
FT   Domain          24..194
FT                   /note= "extracellular domain"
FT   Region          49..71
FT                   /note= "cysteine-rich pseudo-repeat 1"
FT   Region          72..113
FT                   /note= "cysteine-rich pseudo-repeat 1"
FT   Region          114..151
FT                   /note= "cysteine-rich pseudo-repeat 1"
FT   Region          152..194
FT                   /note= "cysteine-rich pseudo-repeat 1"
XX
PN   WO9904001-A1.
XX
PD   28-JAN-1999.
XX
PF   21-JUL-1998;   98WO-US15072.
XX
PR   21-JUL-1997;   97US-0053203.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Farrah TM;
XX
DR   WPI; 1999-132245/11.
DR   N-PSDB; AAX07226.
XX
PT   Novel tumour necrosis factor receptor ZTNFR5  - useful for
PT   regulating maturation of TNF-ligand bearing cells
XX
PS   Claim 1; Page 84-85; 109pp; English.
XX
CC   This polypeptide comprises a new, secreted tumour necrosis factor
CC   receptor (see AAW97749), designated ZTNFR-5.  Novel ZTNFR-5 encoding
CC   polynucleotides and polypeptides were initially identified by
CC   querying an expressed sequence tag (EST) database for sequences
CC   homologous to conserved motifs within the TNF receptor family.
CC   Based on this search, a contig of 16 ESTs (see AAX07226) was
CC   constructed.  ZTNFR-5 polypeptides comprise 4 cysteine-rich repeats
CC   (see also AAW97750-55) that are homologous to other TNF receptors, in
CC   particular the soluble, secreted TNF receptor osteoprotegerin.
CC   ZTNFR-5 polypeptide can be prepared by recombinant methods.  The
CC   polypeptide, especially the extracellular domain, can be used to
CC   generate a soluble variant of ZTNFR-5.  The polypeptides and
CC   nucleic acids can be used to screen for ligands, agonists and
CC   antagonists of ZTNFR-5.  The polypeptides can be used in bone cell
CC   regulation and to regulate the maturation of TNF ligand-bearing
CC   cells such as T- or B-cells, lymphocytes, peripheral blood
CC   mononuclear cells, polymorphonuclear leukocytes, fibroblasts or
CC   haematopoietic cells.
XX
SQ   Sequence   300 AA;

  Query Match            100.0%;  Score 1634;  DB 20;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 8
AAW95082
ID   AAW95082 standard; Protein; 300 AA.
XX
AC   AAW95082;
XX
DT   20-MAY-1999  (first entry)
XX
DE   Orphan receptor (HUMAN NTR-1) polypeptide.
XX
KW   HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;
KW   tumour necrosis factor receptor; muscle disorder; bone mass; screening;
KW   muscle metabolism; binding agent; cognate ligand.
XX
OS   Homo sapiens.
```

XX
PN WO9907738-A2.
XX
PD 18-FEB-1999.
XX
PF 04-AUG-1998; 98WO-US16202.
XX
PR 06-AUG-1997; 97US-0054869.
XX
PA (PROC) PROCTER & GAMBLE CO.
PA (REGE-) REGENERON PHARM INC.
XX
PI Masiakowski PJ, Morris J, Valenzuela DM;
XX
DR WPI; 1999-167365/14.
DR N-PSDB; AAX22300.
XX
PT Novel orphan human receptor polypeptide and nucleic acid - useful as
PT diagnostic reagents and for treatment of muscle disorders
XX
PS Claim 7; Page 21; 23pp; English.
XX
CC This represents a HUMAN NTR-1 polypeptide, a novel orphan receptor. The
CC protein is related to osteoprotegerin (OPG) and to tumour necrosis factor
CC receptor (TNFR). Host cells transformed with a vector comprising the
CC HUMAN NTR-1 nucleic acid are used for the recombinant expression of the
CC protein. HUMAN NTR-1 proteins and antibodies immuno specific for the
CC protein are useful for diagnosis and treatment of humans and animals,
CC especially muscle disorders, as the receptor is involved in regulation of
CC bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful
CC for screening for novel binding agents, and cognate ligands, which may be
CC used to treat disorders associated with HUMAN NTR-1 imbalance.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 20; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.4e-121;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
Db 1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy 61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
Db 61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy 121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
Db 121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy 181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
Db 181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy 241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
Db 241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300

RESULT 9
AAB19335
ID AAB19335 standard; Protein; 300 AA.
XX
AC AAB19335;
XX
DT 19-FEB-2001 (first entry)
XX
DE A full length human FAS Ligand Inhibitory Protein (FLINT).
XX
KW Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;
KW tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;
KW acute respiratory distress syndrome; ulcerative colitis;
KW chronic obstructive pulmonary disease; Crohn's disease.
XX
OS Homo sapiens.
XX
PN WO200058465-A2.
XX
PD 05-OCT-2000.
XX
PF 20-MAR-2000; 2000WO-US06417.
XX
PR 30-MAR-1999; 99US-0126839.
PR 21-JUN-1999; 99US-0140077.
PR 21-JUN-1999; 99US-0140156.
PR 20-OCT-1999; 99US-0160566.
PR 18-FEB-2000; 2000US-0183398.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JE, Micanovic R;
PI Newton CM, Noblitt TW, Rathmachalam R, Tschang SR, Witcher DR;
PI Wroblewski VJ;
XX
DR WPI; 2000-656167/63.
XX
PT FAS Ligand Inhibitory Protein analogs useful for treating abnormal
PT apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,
PT chronic obstructive pulmonary disease ulcerative colitis or Crohn's
PT disease -
XX
PS Disclosure; Page 113-114; 114pp; English.
XX
CC The present sequence represents a full length human FAS Ligand Inhibitory
CC Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor
CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature
CC FLINT protein is modified to produce analogues, which have greater
CC potency, longer in vivo half-lives, decreased aggregation, decreased
CC absorption onto surfaces, increased solubility and improved ease of
CC formulation. The FLINT analogue is useful for treating a patient
CC suffering from disease or condition relating to abnormal apoptosis such
CC as acute lung injury, acute respiratory distress syndrome, pulmonary
CC fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
CC Crohn's disease.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.4e-121;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
Db 1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy 61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
Db 61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy 121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
Db 121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy 181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
Db 181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy 241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
Db 241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300

RESULT 10
AAB28559
ID AAB28559 standard; protein; 300 AA.

XX
AC AAB28559;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human soluble TNF receptor tnfrGT-1.
XX
KW Human; tumour necrosis factor like-1; TNFL1; tumour necrosis factor; TNF;
KW immunosuppressive; antiarthritic; neuroprotective; dermatalogical;
KW antiinflammatory; antidiabetic; cytostatic; osteopathic; gene therapy;
KW colon cancer; rheumatoid arthritis; septic shock; Crohn's disease;
KW osteoporosis; autoimmune disease; myasthenia gravis;
KW insulin-dependent diabetes mellitus.
XX
OS Homo sapiens.
XX
PN WO200060079-A2.
XX
PD 12-OCT-2000.
XX
PF 05-APR-2000; 2000WO-US09058.
XX
PR 05-APR-1999; 99US-0286529.
XX
PA (CHIR) CHIRON CORP.
XX
PI Tribouley C;
XX
DR WPI; 2000-665004/64.
DR N-PSDB; AAC63764.
XX
PT Tumor necrosis factor (TNF) and TNF receptor superfamily protein
PT members TNF-L and TNFR-L, useful for enhancing or decreasing TNF
PT activities such as inducing cell death and lymphoid organogenesis -
XX
PS Claim 1; Page 72; 77pp; English.
XX
CC The present sequence is given in a specification relating to an isolated
CC human protein designated tumour necrosis factor like-1 (TNFL1). It may be
CC used to induce cell death in tumours, to induce apoptosis of activated T
CC cells, to induce inflammation, and to rescue resting T cells from
CC apoptosis. TNF receptors are used to regulate the function of a TNF
CC ligand which plays a role in apoptosis, inflammation, differentiation, or
CC proliferation. Expression of the receptors can also be useful as markers
CC for cancer, especially for colon cancer. Diseases which can be treated
CC using ligands and/or receptors of the TNF/TNFR superfamily include
CC rheumatoid arthritis, cancer, septic shock, Crohn's disease and
CC osteoporosis. The polynucleotides can be used in gene delivery vehicles,
CC for the purpose of delivering a mRNA or oligonucleotide, full-length
CC protein, fusion protein, polypeptide, or ribozyme, or single-chain
CC antibody, into a cell. The newly identified receptor proteins play
CC regulatory roles in cell proliferation and/or differentiation. The
CC receptors can also play a role in the negative regulation of
CC osteoclastogenesis. Soluble TNFR-like receptors can be useful in the
CC neutralisation of TNF or TNF-like ligands. A TNF-L protein can also be
CC used to treat autoimmune diseases (myasthenia gravis and
CC insulin-dependent diabetes mellitus), tumours, and proliferative
CC disorders. A TNF-L or TNFR-L subgenomic polynucleotide can also be
CC delivered to subjects for the purpose of screening test compounds for
CC those which are useful for enhancing transfer of TNF-L subgenomic
CC polynucleotides to the cell or for enhancing subsequent biological
CC effects of TNF-L or TNFR-L subgenomic polynucleotides within the cell.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.4e-121;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
```

RESULT 11
AAB24057
ID AAB24057 standard; Protein; 300 AA.
XX
AC AAB24057;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO212 protein sequence SEQ ID NO:2.
XX
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumourigenesis; identification; cancer; cytostatic;
KW nootropic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocoelic disorder;
KW inflammatory disorder; immunologic disorder.
XX
OS Homo sapiens.
XX
PN WO200053755-A2.
XX
PD 14-SEP-2000.
XX
PF 06-JAN-2000; 2000WO-US00376.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 26-JUL-1999; 99US-0145698.
PR 30-NOV-1999; 99WO-US28313.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2000-572270/53.
DR N-PSDB; AAC58367.
XX
PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer -
XX
PS Claim 61; Fig 2; 286pp; English.
XX
CC The present invention describes an isolated antibody that binds to
CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
CC growth. The PRO polypeptides and nucleotides are useful in the

```
CC   treatment, diagnosis and prevention of cancer. The antibodies and other
CC   anti-tumour compounds maybe used to treat various conditions, including
CC   those characterised by overexpression and/or activation of the amplified
CC   PRO genes. Exemplary conditions or disorders to be treated with such
CC   antibodies and other compounds include benign or malignant tumours
CC   (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
CC   colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
CC   carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
CC   leukaemias and lymphoid malignancies, other disorders such as neuronal,
CC   glial, astrocytal, hypothalamic and other glandular, macrophagal,
CC   epithelial, stromal and blastocoelic disorders, and inflammatory,
CC   angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
CC   primers and hybridisation probes used in the isolation of the human PRO
CC   sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
CC   PRO polynucleotide and protein sequences given in the exemplification of
CC   the present invention.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 21;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 12
AAB33416
ID   AAB33416 standard; Protein; 300 AA.
XX
AC   AAB33416;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human PRO212 protein UNQ186 SEQ ID NO:14.
XX
KW   Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW   dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW   haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW   antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW   antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW   osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW   idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW   systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW   autoimmune thrombocytopaenia; immune-mediated renal disease;
KW   demyelinating disease; hepatobiliary disease; Whipple's disease;
KW   inflammatory bowel disease; gluten-sensitive enteropathy;
KW   autoimmune disease; immune-mediated skin disease; allergic disease;
KW   immunological disease; transplantation associated disease;
KW   graft rejection; graft-versus-host-disease.
XX
OS   Homo sapiens.
XX
PN   WO200053758-A2.
XX
PD   14-SEP-2000.
XX
PF   02-MAR-2000; 2000WO-US05841.
XX
PR   08-MAR-1999;   99WO-US05028.
PR   10-MAR-1999;   99US-0123618.
PR   12-MAR-1999;   99US-0123957.
PR   23-MAR-1999;   99US-0125775.
PR   12-APR-1999;   99US-0128849.
PR   20-APR-1999;   99WO-US08615.
PR   28-APR-1999;   99US-0131445.
PR   04-MAY-1999;   99US-0132371.
PR   14-MAY-1999;   99US-0134287.
PR   02-JUN-1999;   99WO-US12252.
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
PR   28-JUL-1999;   99US-0146222.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   13-SEP-1999;   99WO-US20944.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   05-OCT-1999;   99WO-US23089.
PR   29-OCT-1999;   99US-0162506.
PR   29-NOV-1999;   99WO-US28214.
PR   30-NOV-1999;   99WO-US28313.
PR   30-NOV-1999;   99WO-US28409.
PR   01-DEC-1999;   99WO-US28301.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   02-DEC-1999;   99WO-US28564.
PR   02-DEC-1999;   99WO-US28565.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30999.
PR   30-DEC-1999;   99WO-US31274.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00277.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Goddard A,  Gurney AL,  Hebert C,  Henzel W;
PI   Kabakoff RC,  Lu Y,  Pan J,  Pennica D,  Shelton DL,  Smith V;
PI   Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Yan M;
XX
DR   WPI; 2000-572271/53.
DR   N-PSDB; AAC58581.
XX
PT   Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT   immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT   arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
XX
PS   Claim 33; Fig 6; 309pp; English.
XX
CC   The present invention describes sixty four human PRO proteins which can
CC   be used in the treatment of immune related diseases. The human PRO
CC   proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC   treating and diagnosing immune related disorders. The disorders are
CC   selected from systemic lupus erythematosus, rheumatoid arthritis,
CC   osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC   systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC   syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC   anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC   immune-mediated renal disease, demyelinating diseases of the central
CC   and peripheral nervous systems, hepatobiliary diseases, inflammatory
CC   bowel disease, gluten-sensitive enteropathy and Whipple's disease,
CC   autoimmune or immune-mediated skin diseases, allergic diseases,
CC   immunological diseases of the lung, and transplantation associated
```

```
CC   diseases including graft rejection and graft-versus-host-disease.
CC   AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
CC   in the isolation of human PRO sequences. AAC58579 to AAC58642 and
CC   AAB33414 to AAB33477 represent human PRO polynucleotide and protein
CC   sequences given in the exemplification of the present invention.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 21;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 13
AAB03621
ID   AAB03621 standard; Protein; 300 AA.
XX
AC   AAB03621;
XX
DT   03-JAN-2001  (first entry)
XX
DE   Human Fas ligand inhibitor FLINT.
XX
KW   Human; Fas ligand inhibitor; FLINT; apoptosis; autoimmune disease;
KW   inflammation; infectious disease; ischaemia; Alzheimer's disease;
KW   Parkinson's disease; Crohn's disease; transplantation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1..29
FT                    /label= signal_peptide
FT   Protein          30..300
FT                    /label= mature_FLINT
FT   Domain           1..42
FT                    /label= domain_1
FT   Domain           43..85
FT                    /label= domain_2
FT   Domain           86..122
FT                    /label= domain_3
FT   Domain           123..165
FT                    /label= domain_4
XX
PN   WO200034782-A1.
XX
PD   15-JUN-2000.
XX
PF   07-DEC-1999;   99WO-US28696.
XX
PR   09-DEC-1998;   98US-0111575.
PR   09-DEC-1998;   98US-0111580.
PR   07-JAN-1999;   99US-0115069.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Rosteck PRJ,  Song HY,  Su EW;
XX
DR   WPI; 2000-431379/37.
DR   N-PSDB; AAA53208.
XX
PT   Novel monkey Fas ligand inhibitor polypeptides, useful for treating
PT   inflammatory or autoimmune disease such as rheumatoid arthritis,
PT   infectious diseases such as chronic hepatitis, and
PT   Ischaemia/Re-perfusion conditions -
XX
PS   Claim 19; Page 91-93; 101pp; English.
XX
CC   The present sequence is the protein sequence of the human Fas ligand
CC   inhibitor (FLINT). The FLINT protein is involved in cell-specific
CC   apoptosis, and can be used to treat inflammatory and autoimmune diseases
CC   such as rheumatoid arthritis, inflammatory bowel disease,
CC   graft-versus-host disease, diabetes, psoriasis and Graves' disease,
CC   infectious diseases such as HIV-induced lymphopenia, fulminant viral
CC   hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated
CC   ulceration, ischaemia and reperfusion conditions including acute
CC   myocardial infarction, acute coronary syndrome, congestive heart failure
CC   and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute lung
CC   injury and acute respiratory distress syndrome, Crohn's disease, brain
CC   trauma and injury, chronic glomerulonephritis, osteoporosis, aplastic
CC   anaemia, myelodysplasia, ulcerative colitis, Down's syndrome, and
CC   multiple sclerosis. In addition, the protein and its gene can be used to
CC   prevent apoptosis following organ transplantation.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 21;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 14
AAY97246
ID   AAY97246 standard; Protein; 300 AA.
XX
AC   AAY97246;
XX
DT   19-DEC-2000  (first entry)
XX
DE   M68 TNF receptor related protein.
XX
KW   M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;
KW   receptor; immune response; cell differentiation; ligand; cancer;
KW   bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
KW   Grave's disease; idiopathic myxodema; autoimmune diabetes;
KW   thrombotic thrombocytopenic purpura; multiple sclerosis;
KW   liver diseases; autoimmune gastritis; ulcerative colitis;
```

KW glomerulonephritis; pulmonary fibrosis; heart failure;
KW atherosclerosis; aplastic anaemia; myelodisplastic syndromes;
KW osteoporosis; Alzheimers disease; Parkinsons disease; stroke;
KW myocardial infarction; human.
XX
OS Homo sapiens.
XX
PN WO200046247-A1.
XX
PD 10-AUG-2000.
XX
PF 04-FEB-2000; 2000WO-US03037.
XX
PR 05-FEB-1999; 99US-0118902.
PR 20-DEC-1999; 99US-0172754.
XX
PA (MERI) MERCK & CO INC.
XX
PI Bai C;
XX
DR WPI; 2000-506066/45.
DR N-PSDB; AAA53800, AAA53801, AAA53802.
XX
PT Isolated human M68 nucleic acids and proteins which are part of the
PT tumor necrosis factor receptor (TNFR) family, useful for identifying
PT modulators that may be used to treat various diseases e.g. cancer,
PT osteoporosis, Alzheimer's disease
XX
PS Claim 1; Page 75-76; 80pp; English.
XX
CC The M68 protein is a member of a family of proteins which have
CC roles in immune responses, cell death, cell proliferation and
CC stimulation of cell differentiation. M68 lacks a transmembrane domain
CC and is a secreted factor suggesting that it functions as a natural
CC inhibitor for its ligand. The altered expression pattern of M68 in a
CC multitude of tissues suggests that M68 may play a role in cancer by
CC binding to its ligand and blocking apoptotic cell death induced by
CC such a ligand. This anti-apoptopic role of M68 suggests that
CC modulators of M68 will be useful in treatment of apoptosis-related
CC diseases such as various forms of cancer and various bone disorders.
CC M68 nucleic acids and proteins are therefore useful for treating
CC conditions involving atypical apoptosis and for identifying
CC modulators of M68. Modulators of M68 are useful for treatment of
CC cancer and other diseases associated with abnormal levels of
CC apoptosis including systemic lupus erythematosus, Hashimoto's
CC thyroiditis, Grave's disease, idiopathic myxodema, autoimmune
CC diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,
CC liver diseases, autoimmune gastritis, ulcerative colitis,
CC glomerulonephritis, pulmonary fibrosis, heart failure,
CC atherosclerosis, aplastic anaemia, myelodisplastic syndromes,
CC osteoporosis, Alzheimers disease, Parkinsons disease, stroke, and
CC myocardial infarction.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.4e-121;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
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Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
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Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
```

RESULT 15
AAY90357
ID AAY90357 standard; Protein; 300 AA.
XX
AC AAY90357;
XX
DT 04-DEC-2000 (first entry)
XX
DE Human tumour necrosis factor receptor-6 alpha protein sequence.
XX
KW Human; Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;
KW ocular neovascularisation; solid tumour; malignancy; prostate cancer;
KW breast cancer; colon cancer; diabetic retinopathy; microbial infection;
KW pre-maturity macular degeneration; allergy; inflammation; tissue damage;
KW thyroid associated opthalmopathy; cell damage; parasitic infection;
KW bone disease; osteoporosis; atherosclerosis; cardiovascular disease;
KW neurodegenerative disorder; Alzheimer's disease; immune disorder;
KW graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma;
KW psoriasis; septic shock; ulcerative colitis; therapy.
XX
OS Homo sapiens.
XX
PN WO200052028-A1.
XX
PD 08-SEP-2000.
XX
PF 03-MAR-2000; 2000WO-US05686.
XX
PR 04-MAR-1999; 99US-0121774.
PR 12-MAR-1999; 99US-0124092.
PR 27-APR-1999; 99US-0131279.
PR 30-APR-1999; 99US-0131964.
PR 02-AUG-1999; 99US-0146371.
PR 01-DEC-1999; 99US-0168235.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Gentz RL, Ni J, Ebner R, Yu G, Ruben SM, Feng P;
XX
DR WPI; 2000-572174/53.
DR N-PSDB; AAA37772.
XX
PT Nucleic acids encoding human tumour necrosis factor receptor (TNFR)
PT proteins TNFR-6alpha and TNFR-6beta, useful for treating e.g.
PT Alzheimer's disease, osteoporosis and graft rejection -
XX
PS Claim 20; Fig 1; 332pp; English.
XX
CC This sequence represents the human tumour necrosis factor receptor 6
CC alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA
CC and protein sequences can be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate TNFR expression. The
CC nucleic acids, polypeptides, antibodies, agonists and antagonists against
CC them may be used for the treatment of a range of conditions such as
CC disorders associated with neovascularisation (especially ocular
CC neovascularisation) (such as solid tumours and malignancies (e.g.
CC prostate cancer, breast cancer and colon cancer), diabetic retinopathy
CC and pre-maturity macular degeneration), allergies, inflammation,
CC thyroid associated opthalmopathy tissue/cell damage, wounds, microbial
CC and parasitic infections, bone disease (e.g. osteoporosis),
CC atherosclerosis, pain, cardiovascular disease (e.g. stroke),
CC neurodegenerative disorders (e.g. Alzheimer's disease), immune
CC disorders (e.g. graft rejection), rheumatism, liver disease,
CC autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative
CC colitis.
XX

SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 21; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.4e-121;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
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Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
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Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
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Search completed: July 16, 2003, 19:36:59
Job time : 40 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 17, 2003, 15:22:24 ; Search time 38 Seconds
(without alignments)
1051.979 Million cell updates/sec

Title: US-09-935-727-2
Perfect score: 1634
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 73

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1634	100.0	300	19	AAW66102	Amino acid sequenc
2	1634	100.0	300	19	AAW63622	Human tumour necro
3	1634	100.0	300	20	AAY03099	Human lung TNF-rec
4	1634	100.0	300	20	AAY42182	Human FLINT #1 pro
5	1634	100.0	300	20	AAY17479	Mammalian tumour n
6	1634	100.0	300	20	AAY06817	Human DcR3 polypep
7	1634	100.0	300	20	AAW97749	Human tumour necro
8	1634	100.0	300	20	AAW95082	Orphan receptor (H
9	1634	100.0	300	21	AAB19335	A full length huma
10	1634	100.0	300	21	AAB28559	Human soluble TNF
11	1634	100.0	300	21	AAB24057	Human PRO212 prote
12	1634	100.0	300	21	AAB33416	Human PRO212 prote
13	1634	100.0	300	21	AAB03621	Human Fas ligand i
14	1634	100.0	300	21	AAY97246	M68 TNF receptor r
15	1634	100.0	300	21	AAY90357	Human tumour necro
16	1634	100.0	300	21	AAB24395	Human PRO212 prote
17	1634	100.0	300	21	AAY96596	Human FLINT. Homo
18	1634	100.0	300	22	AAE03568	Human native fas l
19	1634	100.0	300	22	AAB74466	Human FLINT native
20	1634	100.0	300	22	AAB71754	Human NTR3. Homo
21	1634	100.0	300	22	AAB48161	Human PRO212 polyp
22	1634	100.0	300	22	AAB50903	Human PRO212 prote
23	1634	100.0	300	23	AAE14579	Human native FLINT
24	1634	100.0	300	23	AAE20848	Human tumour necro
25	1634	100.0	341	22	AAG73740	Human colon cancer
26	1620	99.1	300	21	AAY77458	Human TNF receptor
27	1619	99.1	300	21	AAB19710	Human FAS ligand i
28	1619	99.1	300	21	AAY96597	Human FLINT. Homo
29	1619	99.1	300	22	AAE03570	Human fas ligand i
30	1619	99.1	300	22	AAB83950	Amino acid sequenc
31	1619	99.1	300	22	AAB68045	Amino acid sequenc
32	1619	99.1	300	22	AAB68048	Amino acid sequenc
33	1619	99.1	300	23	AAE14580	Human FLINT analog
34	1610	98.5	302	20	AAY42183	Human FLINT #2 pro
35	1532	93.8	326	23	ABP41980	Human ovarian anti
36	1509	92.4	300	21	AAB03623	Human Fas ligand i
37	1502	91.9	300	21	AAB03622	Monkey Fas ligand
38	1502	91.9	300	21	AAB03624	Human Fas ligand i
39	1491	91.2	271	20	AAY42184	Human mFLINT #1 pr
40	1491	91.2	271	21	AAB19334	A mature human FAS
41	1491	91.2	271	21	AAB19705	Human FAS ligand i
42	1491	91.2	271	21	AAY97247	M68 TNF receptor r
43	1491	91.2	271	21	AAY96598	Human mature FLINT
44	1491	91.2	271	22	AAE03567	Human mature fas l
45	1491	91.2	271	22	AAB68044	Amino acid sequenc
46	1491	91.2	271	22	AAB68047	Amino acid sequenc
47	1491	91.2	271	22	AAB74465	Human FLINT mature
48	1491	91.2	271	23	AAE14578	Human mature FLINT
49	1487	91.0	271	21	AAB19709	Protease-resistant
50	1487	91.0	271	22	AAE03571	Human mature fas l
51	1487	91.0	271	22	AAB74467	Human FLINT mature
52	1487	91.0	271	23	AAE14581	Human protease-res
53	1486	90.9	271	22	AAE03584	Human mature fas l
54	1486	90.9	271	23	AAE14582	Human protease-res
55	1485	90.9	271	21	AAY96599	Human mature FLINT
56	1485	90.9	271	23	AAE14583	Human protease-res
57	1485	90.9	271	23	AAE14584	Human protease-res
58	1485	90.9	271	23	AAE14586	Human protease-res
59	1485	90.9	271	23	AAE14590	Human protease-res
60	1484	90.8	271	23	AAE14585	Human protease-res
61	1484	90.8	271	23	AAE14588	Human protease-res
62	1483	90.8	271	23	AAE14587	Human protease-res
63	1481	90.6	271	21	AAB19708	Protease-resistant
64	1481	90.6	271	23	AAE14589	Human protease-res
65	1475	90.3	271	21	AAB19706	Protease-resistant
66	1471	90.0	271	22	AAB68046	Amino acid sequenc
67	1467	89.8	271	21	AAB19707	Protease-resistant
68	1467	89.8	273	20	AAY42185	Human mFLINT #2 pr
69	1362	83.4	245	20	AAY28449	A human tumour nec
70	1177	72.0	211	21	AAB28560	Human soluble TNF
71	1153	70.6	215	20	AAW93585	Human hAPO6 protei
72	841	51.5	153	20	AAY22222	Human TNFR superfa
73	841	51.5	153	21	AAB28554	Human TNFR soluble

ALIGNMENTS

RESULT 1
AAW66102
ID AAW66102 standard; Protein; 300 AA.
XX
AC AAW66102;

XX
DT 02-DEC-1998 (first entry)
XX
DE Amino acid sequence of tumour necrosis related receptor (TR4).
XX
KW Human; tumour necrosis related receptor; TR4; agonist; antagonist;
KW inhibition; chronic; acute; inflammation; arthritis; septicaemia;
KW autoimmune disease; transplant rejection; stroke; cancer;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN EP861850-A1.
XX
PD 02-SEP-1998.
XX
PF 20-JAN-1998; 98EP-0300382.
XX
PR 04-FEB-1997; 97US-0794796.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Emery J, Tan KB, Truneh A, Young PR;
XX
DR WPI; 1998-508248/44.
DR N-PSDB; AAV07654.
XX
PT New DNA encoding tumour necrosis related receptor - used to treat
PT and prevent e.g. inflammation, arthritis, septicaemia, autoimmune
PT diseases, transplant rejection, infection, stroke, ischaemia, ARDS,
PT restenosis, AIDS, bone disorders and cancer
XX
PS Claim 1; Fig 1; 21pp; English.
XX
CC This is the amino acid sequence of the human tumour necrosis related
CC receptor (TR4), used in the method of the invention. The TR4 protein
CC or its agonist can be used to treat a subject in need of enhanced
CC TR4 polypeptide activity. The antagonist is used to inhibit TR4
CC polypeptide activity. The active agents can be used for the
CC treatment and prevention of diseases such as chronic and acute
CC inflammation, arthritis, septicaemia, autoimmune diseases, transplant
CC rejection, stroke, cancer, Alzheimer's disease.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 19; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.4e-121;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
```

RESULT 2
AAW63622
ID AAW63622 standard; Protein; 300 AA.

XX
AC AAW63622;
XX
DT 26-OCT-1998 (first entry)
XX
DE Human tumour necrosis factor receptor-6 alpha protein.
XX
KW Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
KW endothelial cells; keratinocytes; normal prostate; apoptosis;
KW prostate tumour tissue.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Protein 31..300
FT /note= "TNFR-6 alpha"
FT Region 31..282
FT /note= "Soluble extracellular domain"
XX
PN WO9830694-A2.
XX
PD 16-JUL-1998.
XX
PF 13-JAN-1998; 98WO-US00153.
XX
PR 14-JAN-1997; 97US-0035496.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;
XX
DR WPI; 1998-399142/34.
DR N-PSDB; AAV39085.
XX
PT Human tumour necrosis factor receptors 6-alpha and 6-beta - used in
PT the diagnosis of immune system-related disorder(s)
XX
PS Claim 20; Fig 1; 91pp; English.
XX
CC The present sequence represents the human tumour necrosis factor
CC receptor-6 alpha (TNFR-6 alpha) protein. The invention also provides
CC for the TNFR-6 beta protein (AAW63623). TNFR-6 alpha and TNFR-6 beta
CC are members of the tumour necrosis factor receptor (TNFR) family. TNFRs
CC are expressed in endothelial cells, keratinocytes, normal prostate and
CC prostate tumour tissue. For a number of disorders of these cells,
CC particularly of the immune system, substantially altered (whether
CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene
CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta
CC polypeptides, nucleic acids and antibodies are claimed to be useful in
CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and
CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are
CC also claimed to be useful for identifying ligands which may be useful
CC in the treatment of apoptosis related disorders.
XX
SQ Sequence 300 AA;

Query Match 100.0%; Score 1634; DB 19; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.4e-121;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
```

```
Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 3
AAY03099
ID   AAY03099 standard; Protein; 300 AA.
XX
AC   AAY03099;
XX
DT   09-DEC-1999  (first entry)
XX
DE   Human lung TNF-receptor protein.
XX
KW   Tumour necrosis factor; TNF; TNF receptor; human; lung; gene therapy;
KW   detection; immunoassay; diagnosis; disease; immune system; tumour;
KW   osteogenic system; cardiovascular system; central nervous system; asthma;
KW   peripheral nervous systems; transplant incompatibility; antitumor;
KW   rheumatoid arthritis; antiasthmatic; antiarthritic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             134..1036
FT                   /*tag=  a
FT                   /product= "TNF-receptor"
XX
PN   DE19809978-A1.
XX
PD   16-SEP-1999.
XX
PF   09-MAR-1998;   98DE-1009978.
XX
PR   09-MAR-1998;   98DE-1009978.
XX
PA   (BADI ) BASF AG.
XX
PI   Kroeger B;
XX
DR   WPI; 1999-519473/44.
DR   N-PSDB; AAZ09998.
XX
PT   New soluble member of tumor necrosis factor receptor family, useful for
PT   identification specific modulators and for treating disease e.g. tumors
PT   -
XX
PS   Claim 1; Page 8-9; 10pp; German.
XX
CC   This invention describes a novel tumour necrosis factor (TNF) receptor
CC   (I) isolated from human lung tissue. (I) is used: (i) to raise specific
CC   antibodies (Ab); (ii) to screen for specific (ant)agonists or ligands
CC   (A), potential therapeutic agents; and (iii) therapeutically (optionally
CC   expressed from a gene therapy vector) in conditions associated with a
CC   deficit of (I). Ab are used: (a) for qualitative or quantitative
CC   detection of (I) in standard immunoassays (for diagnosis of disease, or
CC   susceptibility, or for monitoring); and (b) as therapeutic inhibitors in
CC   cases where (I) is overexpressed. Nucleic acid (II) that encodes (I) is
CC   used: (A) for recombinant production of (I); (B) also its oligonucleotide
CC   fragments, in standard hybridization and/or amplification assays; (C) as
CC   source of antisense molecules or ribozymes; and (D) to produce transgenic
CC   animals (for studying (patho)physiology of (I)). Diseases possibly
CC   associated with under- or over-expression of (I) are those of the immune,
CC   osteogenic, cardiovascular and central or peripheral nervous systems,
CC   tumors, transplant incompatibility, asthma and rheumatoid arthritis. The
CC   products of the invention have antitumor, antiasthmatic and
CC   antiarthritic activity. This sequence represents the TNF-receptor of the
CC   invention.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 20;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 4
AAY42182
ID   AAY42182 standard; Protein; 300 AA.
XX
AC   AAY42182;
XX
DT   17-DEC-1999  (first entry)
XX
DE   Human FLINT #1 protein sequence.
XX
KW   Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
KW   apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW   sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW   reperfusion-associated injury; aplastic anaemia; differentiation;
KW   growth; myelodysplastic syndrome; pancytopenic condition;
KW   myocardial ischaemia.
XX
OS   Homo sapiens.
XX
PN   WO9950413-A2.
XX
PD   07-OCT-1999.
XX
PF   30-MAR-1999;   99WO-US06797.
XX
PR   30-MAR-1998;   98US-0079856.
PR   20-MAY-1998;   98US-0086074.
PR   09-SEP-1998;   98US-0099643.
PR   17-DEC-1998;   98US-0112577.
PR   18-DEC-1998;   98US-0112703.
PR   18-DEC-1998;   98US-0112933.
PR   22-DEC-1998;   98US-0113407.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Bumol TF,  Dou S,  Glasebrook AL,  Gould KE,  Hale JE,  Heuer JG;
PI   Hui KY,  Kharitonenkov A,  Mizrahi J,  Na S,  Noblitt TW,  Reidy CA;
PI   Song HY,  Wang J,  Wu X,  Zuckerman SH;
XX
DR   WPI; 1999-591319/50.
DR   N-PSDB; AAZ25375.
XX
PT   Use of mature FLINT for treating acute liver failure, inflammation,
PT   cancer, and diabetes  - by prevention of FasL-Fas mediated apoptotic
PT   and proinflammatory activity
XX
```

```
PS   Claim 30; Fig 1; 99pp; English.
XX
CC   The present invention describes therapeutic applications of mature FLINT
CC   (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
CC   (mFLINT), which is a member of the tumour necrosis factor receptor
CC   superfamily, is used for treating acute liver failure, inflammation of
CC   the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
CC   with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
CC   injury or disorder such as hypercoagulation (including use with
CC   thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
CC   or disorder, Type I diabetes, cancer, cell damage or damage to an
CC   innocent bystander tissue that is induced by a chemotherapeutic agent or
CC   therapeutic irradiation, treating haematopoietic progenitor cells that
CC   have been exposed to therapeutic radiation or chemotherapy, aplastic
CC   anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
CC   also used for promoting the growth or differentiation of a haematopoietic
CC   progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
CC   resulting from abnormal myocardial ischaemia. The present sequence
CC   represents human FLINT.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 20;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 5
AAY17479
ID   AAY17479 standard; Protein; 300 AA.
XX
AC   AAY17479;
XX
DT   02-AUG-1999  (first entry)
XX
DE   Mammalian tumour necrosis factor receptor OPG-2.
XX
KW   Tumour necrosis factor receptor; TNF receptor; OPG-2; Paget's disease;
KW   osteopenic disorder; osteoclast activity; primary osteoporosis;
KW   hyperglycaemia; osteolytic metastasis; immune response; cancer.
XX
OS   Mammalia.
XX
PN   WO9926977-A1.
XX
PD   03-JUN-1999.
XX
PF   24-NOV-1998;   98WO-US25065.
XX
PR   17-FEB-1998;   98US-0074896.
PR   24-NOV-1997;   97US-0066446.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Tschopp J;
XX
DR   WPI; 1999-347693/29.
DR   N-PSDB; AAX76052.
XX
PT   New tumour necrosis factor family receptor OPG-2
XX
PS   Claim 1; Page 18; 22pp; English.
XX
CC   The present sequence represents a mammalian tumour necrosis factor
CC   receptor, designated OPG-2. OPG-2, is a member of the tumour necrosis
CC   factor receptor family, and can be used: (i) to raise specific
CC   antibodies (Ab), (ii) to treat osteopenic disorders associated with
CC   excessive osteoclast activity, e.g. primary osteoporosis, Paget's
CC   disease, hyperglycaemia of malignancy, or osteolytic metastases; (iii)
CC   for affinity purification of cognate ligands, and (iv) to screen for
CC   ligands (antagonists or agonists). Ab, or other OPG-2 blocking agents
CC   such as soluble forms of the protein, are used to prevent, or reduce
CC   severity of, an immune response, and for treating cancer. They can also
CC   be used in diagnostic assays. The nucleic acid sequence encoding OPG-2
CC   can be used as a probe to isolate related sequences from other species.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 20;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 6
AAY06817
ID   AAY06817 standard; Protein; 300 AA.
XX
AC   AAY06817;
XX
DT   24-JUN-1999  (first entry)
XX
DE   Human DcR3 polypeptide.
XX
KW   DcR3 polypeptide; tumour necrosis factor receptor; TNFR; Fas ligand;
KW   apoptosis; T cell mediated immune response; allergy; asthma; cancer;
KW   rheumatoid arthritis; Crohn's disease; guest vs. host disease; human;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO9914330-A1.
XX
PD   25-MAR-1999.
XX
PF   18-SEP-1998;   98WO-US19661.
XX
```

```
PR   30-JUL-1998;   98US-0094640.
PR   18-SEP-1997;   97US-0059288.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Botstein D,  Dodge KH,  Goddard A,  Gurney AL;
PI   Kim KJ,  Lawrence DA,  Pitti R,  Roy MA,  Tumas DB;
PI   Wood WI;
XX
DR   WPI; 1999-244032/20.
DR   N-PSDB; AAX32744.
XX
PT   DcR3 polypeptide related to tumor necrosis factor receptor
XX
PS   Claim 5; Fig 1; 88pp; English.
XX
CC   This represents a human DcR3 polypeptide, a homologue of tumour necrosis
CC   factor receptor (TNFR) polypeptide. Host cells containing a vector
CC   comprising the DcR3 nucleic acid can be used for the recombinant
CC   expression of the protein. DcR3 binds to Fas ligand, so it (or its
CC   chimeras) are useful for modulating apoptosis in mammalian cells, also
CC   other Fas-ligand induced activities, particularly to inhibit T cell
CC   mediated immune responses, e.g. in treatment of allergy, asthma,
CC   rheumatoid arthritis, Crohn's disease, guest vs. host disease etc. DcR3
CC   may also be used to identify specific binding proteins, potential
CC   inhibitors. Antibodies against DcR3 are used to treat cancer,
CC   specifically of the lung and colon, also in diagnosis and for affinity
CC   purification of the protein. Detecting mutations in the gene for DcR3 is
CC   also used to diagnose cancer, or predisposition to it. DcR3 nucleic acid
CC   is useful as hybridization probe to detect genomic or related sequences;
CC   for chromosome and gene mapping; as source of antisense sequences; for
CC   expression of recombinant DcR3 and to generate transgenic animals (for
CC   development and screening of therapeutic agents), also for in vivo or
CC   ex vivo gene therapy.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 20;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 7
AAW97749
ID   AAW97749 standard; Protein; 300 AA.
XX
AC   AAW97749;
XX
DT   21-MAY-1999  (first entry)
XX
DE   Human tumour necrosis factor receptor ZTNFR-5.
XX
KW   ZTNFR-5; tumour necrosis factor receptor; TNFR; human;
KW   cell maturation; bone cell regulation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..23
FT                   /note= "signal peptide"
FT   Protein         24..300
FT                   /note= "mature protein"
FT   Domain          24..194
FT                   /note= "extracellular domain"
FT   Region          49..71
FT                   /note= "cysteine-rich pseudo-repeat 1"
FT   Region          72..113
FT                   /note= "cysteine-rich pseudo-repeat 1"
FT   Region          114..151
FT                   /note= "cysteine-rich pseudo-repeat 1"
FT   Region          152..194
FT                   /note= "cysteine-rich pseudo-repeat 1"
XX
PN   WO9904001-A1.
XX
PD   28-JAN-1999.
XX
PF   21-JUL-1998;   98WO-US15072.
XX
PR   21-JUL-1997;   97US-0053203.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Farrah TM;
XX
DR   WPI; 1999-132245/11.
DR   N-PSDB; AAX07226.
XX
PT   Novel tumour necrosis factor receptor ZTNFR5  - useful for
PT   regulating maturation of TNF-ligand bearing cells
XX
PS   Claim 1; Page 84-85; 109pp; English.
XX
CC   This polypeptide comprises a new, secreted tumour necrosis factor
CC   receptor (see AAW97749), designated ZTNFR-5.  Novel ZTNFR-5 encoding
CC   polynucleotides and polypeptides were initially identified by
CC   querying an expressed sequence tag (EST) database for sequences
CC   homologous to conserved motifs within the TNF receptor family.
CC   Based on this search, a contig of 16 ESTs (see AAX07226) was
CC   constructed.  ZTNFR-5 polypeptides comprise 4 cysteine-rich repeats
CC   (see also AAW97750-55) that are homologous to other TNF receptors, in
CC   particular the soluble, secreted TNF receptor osteoprotegerin.
CC   ZTNFR-5 polypeptide can be prepared by recombinant methods.  The
CC   polypeptide, especially the extracellular domain, can be used to
CC   generate a soluble variant of ZTNFR-5.  The polypeptides and
CC   nucleic acids can be used to screen for ligands, agonists and
CC   antagonists of ZTNFR-5.  The polypeptides can be used in bone cell
CC   regulation and to regulate the maturation of TNF ligand-bearing
CC   cells such as T- or B-cells, lymphocytes, peripheral blood
CC   mononuclear cells, polymorphonuclear leukocytes, fibroblasts or
CC   haematopoietic cells.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 20;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
```

```
Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
```

RESULT 8
AAW95082
ID AAW95082 standard; Protein; 300 AA.
XX
AC AAW95082;
XX
DT 20-MAY-1999 (first entry)
XX
DE Orphan receptor (HUMAN NTR-1) polypeptide.
XX
KW HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;
KW tumour necrosis factor receptor; muscle disorder; bone mass; screening;
KW muscle metabolism; binding agent; cognate ligand.
XX
OS Homo sapiens.
XX
PN WO9907738-A2.
XX
PD 18-FEB-1999.
XX
PF 04-AUG-1998; 98WO-US16202.
XX
PR 06-AUG-1997; 97US-0054869.
XX
PA (PROC) PROCTER & GAMBLE CO.
PA (REGE-) REGENERON PHARM INC.
XX
PI Masiakowski PJ, Morris J, Valenzuela DM;
XX
DR WPI; 1999-167365/14.
DR N-PSDB; AAX22300.
XX
PT Novel orphan human receptor polypeptide and nucleic acid - useful as
PT diagnostic reagents and for treatment of muscle disorders
XX
PS Claim 7; Page 21; 23pp; English.
XX
CC This represents a HUMAN NTR-1 polypeptide, a novel orphan receptor. The
CC protein is related to osteoprotegerin (OPG) and to tumour necrosis factor
CC receptor (TNFR). Host cells transformed with a vector comprising the
CC HUMAN NTR-1 nucleic acid are used for the recombinant expression of the
CC protein. HUMAN NTR-1 proteins and antibodies immuno specific for the
CC protein are useful for diagnosis and treatment of humans and animals,
CC especially muscle disorders, as the receptor is involved in regulation of
CC bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful
CC for screening for novel binding agents, and cognate ligands, which may be
CC used to treat disorders associated with HUMAN NTR-1 imbalance.
XX
SQ Sequence 300 AA;

```
  Query Match             100.0%;  Score 1634;  DB 20;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
```

RESULT 9
AAB19335
ID AAB19335 standard; Protein; 300 AA.
XX
AC AAB19335;
XX
DT 19-FEB-2001 (first entry)
XX
DE A full length human FAS Ligand Inhibitory Protein (FLINT).
XX
KW Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;
KW tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;
KW acute respiratory distress syndrome; ulcerative colitis;
KW chronic obstructive pulmonary disease; Crohn's disease.
XX
OS Homo sapiens.
XX
PN WO200058465-A2.
XX
PD 05-OCT-2000.
XX
PF 20-MAR-2000; 2000WO-US06417.
XX
PR 30-MAR-1999; 99US-0126839.
PR 21-JUN-1999; 99US-0140077.
PR 21-JUN-1999; 99US-0140156.
PR 20-OCT-1999; 99US-0160566.
PR 18-FEB-2000; 2000US-0183398.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JE, Micanovic R;
PI Newton CM, Noblitt TW, Rathmachalam R, Tschang SR, Witcher DR;
PI Wroblewski VJ;
XX
DR WPI; 2000-656167/63.
XX
PT FAS Ligand Inhibitory Protein analogs useful for treating abnormal
PT apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,
PT chronic obstructive pulmonary disease ulcerative colitis or Crohn's
PT disease -
XX
PS Disclosure; Page 113-114; 114pp; English.
XX
CC The present sequence represents a full length human FAS Ligand Inhibitory
CC Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor
CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature
CC FLINT protein is modified to produce analogues, which have greater
CC potency, longer in vivo half-lives, decreased aggregation, decreased
CC absorption onto surfaces, increased solubility and improved ease of
CC formulation. The FLINT analogue is useful for treating a patient
CC suffering from disease or condition relating to abnormal apoptosis such
CC as acute lung injury, acute respiratory distress syndrome, pulmonary
CC fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
CC Crohn's disease.
XX
SQ Sequence 300 AA;

```
  Query Match           100.0%;  Score 1634;  DB 21;  Length 300;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
```

```
RESULT 10
AAB28559
ID   AAB28559 standard; protein; 300 AA.
XX
AC   AAB28559;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human soluble TNF receptor tnfrGT-1.
XX
KW   Human; tumour necrosis factor like-1; TNFL1; tumour necrosis factor; TNF;
KW   immunosuppressive; antiarthritic; neuroprotective; dermatalogical;
KW   antiinflammatory; antidiabetic; cytostatic; osteopathic; gene therapy;
KW   colon cancer; rheumatoid arthritis; septic shock; Crohn's disease;
KW   osteoporosis; autoimmune disease; myasthenia gravis;
KW   insulin-dependent diabetes mellitus.
XX
OS   Homo sapiens.
XX
PN   WO200060079-A2.
XX
PD   12-OCT-2000.
XX
PF   05-APR-2000; 2000WO-US09058.
XX
PR   05-APR-1999;   99US-0286529.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Tribouley C;
XX
DR   WPI; 2000-665004/64.
DR   N-PSDB; AAC63764.
XX
PT   Tumor necrosis factor (TNF) and TNF receptor superfamily protein
PT   members TNF-L and TNFR-L, useful for enhancing or decreasing TNF
PT   activities such as inducing cell death and lymphoid organogenesis -
XX
PS   Claim 1; Page 72; 77pp; English.
XX
CC   The present sequence is given in a specification relating to an isolated
CC   human protein designated tumour necrosis factor like-1 (TNFL1). It may be
CC   used to induce cell death in tumours, to induce apoptosis of activated T
CC   cells, to induce inflammation, and to rescue resting T cells from
CC   apoptosis. TNF receptors are used to regulate the function of a TNF
CC   ligand which plays a role in apoptosis, inflammation, differentiation, or
CC   proliferation. Expression of the receptors can also be useful as markers
CC   for cancer, especially for colon cancer. Diseases which can be treated
CC   using ligands and/or receptors of the TNF/TNFR superfamily include
CC   rheumatoid arthritis, cancer, septic shock, Crohn's disease and
CC   osteoporosis. The polynucleotides can be used in gene delivery vehicles,
CC   for the purpose of delivering a mRNA or oligonucleotide, full-length
CC   protein, fusion protein, polypeptide, or ribozyme, or single-chain
CC   antibody, into a cell. The newly identified receptor proteins play
CC   regulatory roles in cell proliferation and/or differentiation. The
CC   receptors can also play a role in the negative regulation of
CC   osteoclastogenesis. Soluble TNFR-like receptors can be useful in the
CC   neutralisation of TNF or TNF-like ligands. A TNF-L protein can also be
CC   used to treat autoimmune diseases (myasthenia gravis and
CC   insulin-dependent diabetes mellitus), tumours, and proliferative
CC   disorders. A TNF-L or TNFR-L subgenomic polynucleotide can also be
CC   delivered to subjects for the purpose of screening test compounds for
CC   those which are useful for enhancing transfer of TNF-L subgenomic
CC   polynucleotides to the cell or for enhancing subsequent biological
CC   effects of TNF-L or TNFR-L subgenomic polynucleotides within the cell.
XX
SQ   Sequence   300 AA;
```

```
  Query Match           100.0%;  Score 1634;  DB 21;  Length 300;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
```

```
RESULT 11
AAB24057
ID   AAB24057 standard; Protein; 300 AA.
XX
AC   AAB24057;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human PRO212 protein sequence SEQ ID NO:2.
XX
KW   Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW   proliferation; tumourigenesis; identification; cancer; cytostatic;
KW   nootropic; neuroprotective; antiinflammatory; immunosuppressive;
KW   immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW   neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
KW   hypothalamic disorder; glandular disorder; macrophagal disorder;
KW   epithelial disorder; stromal disorder; blastocoelic disorder;
KW   inflammatory disorder; immunologic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200053755-A2.
XX
PD   14-SEP-2000.
XX
PF   06-JAN-2000; 2000WO-US00376.
XX
PR   08-MAR-1999;   99WO-US05028.
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PR   02-JUN-1999;   99WO-US12252.
PR   23-JUN-1999;   99US-0141037.
PR   07-JUL-1999;   99US-0143048.
PR   26-JUL-1999;   99US-0145698.
PR   30-NOV-1999;   99WO-US28313.
PR   20-DEC-1999;   99WO-US30911.
PR   05-JAN-2000; 2000WO-US00219.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Goddard A,  Gurney AL,  Hillan KJ,  Roy MA;
PI   Watanabe CK,  Wood WI;
XX
DR   WPI; 2000-572270/53.
DR   N-PSDB; AAC58367.
XX
PT   Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT   treatment, diagnosis and prevention of cancer -
XX
PS   Claim 61; Fig 2; 286pp; English.
XX
CC   The present invention describes an isolated antibody  that binds to
CC   one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
CC   PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
CC   PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
CC   PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
CC   PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
CC   growth. The PRO polypeptides and nucleotides are useful in the
CC   treatment, diagnosis and prevention of cancer. The antibodies and other
CC   anti-tumour compounds maybe used to treat various conditions, including
CC   those characterised by overexpression and/or activation of the amplified
CC   PRO genes. Exemplary conditions or disorders to be treated with such
CC   antibodies and other compounds include benign or malignant tumours
CC   (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
CC   colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
CC   carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
CC   leukaemias and lymphoid malignancies, other disorders such as neuronal,
CC   glial, astrocytal, hypothalamic and other glandular, macrophagal,
CC   epithelial, stromal and blastocoelic disorders, and inflammatory,
CC   angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
CC   primers and hybridisation probes used in the isolation of the human PRO
CC   sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
CC   PRO polynucleotide and protein sequences given in the exemplification of
CC   the present invention.
XX
SQ   Sequence   300 AA;

  Query Match           100.0%;  Score 1634;  DB 21;  Length 300;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300

RESULT 12
AAB33416
ID   AAB33416 standard; Protein; 300 AA.
XX
AC   AAB33416;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human PRO212 protein UNQ186 SEQ ID NO:14.
XX
KW   Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW   dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW   haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW   antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW   antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW   osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW   idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW   systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW   autoimmune thrombocytopaenia; immune-mediated renal disease;
KW   demyelinating disease; hepatobiliary disease; Whipple's disease;
KW   inflammatory bowel disease; gluten-sensitive enteropathy;
KW   autoimmune disease; immune-mediated skin disease; allergic disease;
KW   immunological disease; transplantation associated disease;
KW   graft rejection; graft-versus-host-disease.
XX
OS   Homo sapiens.
XX
PN   WO200053758-A2.
XX
PD   14-SEP-2000.
XX
PF   02-MAR-2000; 2000WO-US05841.
XX
PR   08-MAR-1999;   99WO-US05028.
PR   10-MAR-1999;   99US-0123618.
PR   12-MAR-1999;   99US-0123957.
PR   23-MAR-1999;   99US-0125775.
PR   12-APR-1999;   99US-0128849.
PR   20-APR-1999;   99WO-US08615.
PR   28-APR-1999;   99US-0131445.
PR   04-MAY-1999;   99US-0132371.
PR   14-MAY-1999;   99US-0134287.
PR   02-JUN-1999;   99WO-US12252.
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
PR   28-JUL-1999;   99US-0146222.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   13-SEP-1999;   99WO-US20944.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   05-OCT-1999;   99WO-US23089.
PR   29-OCT-1999;   99US-0162506.
PR   29-NOV-1999;   99WO-US28214.
PR   30-NOV-1999;   99WO-US28313.
PR   30-NOV-1999;   99WO-US28409.
PR   01-DEC-1999;   99WO-US28301.
PR   01-DEC-1999;   99WO-US28634.
PR   02-DEC-1999;   99WO-US28551.
PR   02-DEC-1999;   99WO-US28564.
PR   02-DEC-1999;   99WO-US28565.
PR   16-DEC-1999;   99WO-US30095.
PR   20-DEC-1999;   99WO-US30999.
PR   30-DEC-1999;   99WO-US31274.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00277.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
XX
PA   (GETH ) GENENTECH INC.
```

```
XX
PI   Ashkenazi AJ,  Baker KP,  Goddard A,  Gurney AL,  Hebert C,  Henzel W;
PI   Kabakoff RC,  Lu Y,  Pan J,  Pennica D,  Shelton DL,  Smith V;
PI   Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Yan M;
XX
DR   WPI; 2000-572271/53.
DR   N-PSDB; AAC58581.
XX
PT   Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT   immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT   arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
XX
PS   Claim 33; Fig 6; 309pp; English.
XX
CC   The present invention describes sixty four human PRO proteins which can
CC   be used in the treatment of immune related diseases. The human PRO
CC   proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC   treating and diagnosing immune related disorders. The disorders are
CC   selected from systemic lupus erythematosus, rheumatoid arthritis,
CC   osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC   systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC   syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC   anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC   immune-mediated renal disease, demyelinating diseases of the central
CC   and peripheral nervous systems, hepatobiliary diseases, inflammatory
CC   bowel disease, gluten-sensitive enteropathy and Whipple's disease,
CC   autoimmune or immune-mediated skin diseases, allergic diseases,
CC   immunological diseases of the lung, and transplantation associated
CC   diseases including graft rejection and graft-versus-host-disease.
CC   AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
CC   in the isolation of human PRO sequences. AAC58579 to AAC58642 and
CC   AAB33414 to AAB33477 represent human PRO polynucleotide and protein
CC   sequences given in the exemplification of the present invention.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 21;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 13
AAB03621
ID   AAB03621 standard; Protein; 300 AA.
XX
AC   AAB03621;
XX
DT   03-JAN-2001  (first entry)
XX
DE   Human Fas ligand inhibitor FLINT.
XX
KW   Human; Fas ligand inhibitor; FLINT; apoptosis; autoimmune disease;
KW   inflammation; infectious disease; ischaemia; Alzheimer's disease;
KW   Parkinson's disease; Crohn's disease; transplantation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..29
FT                   /label= signal_peptide
FT   Protein         30..300
FT                   /label= mature_FLINT
FT   Domain          1..42
FT                   /label= domain_1
FT   Domain          43..85
FT                   /label= domain_2
FT   Domain          86..122
FT                   /label= domain_3
FT   Domain          123..165
FT                   /label= domain_4
XX
PN   WO200034782-A1.
XX
PD   15-JUN-2000.
XX
PF   07-DEC-1999;   99WO-US28696.
XX
PR   09-DEC-1998;   98US-0111575.
PR   09-DEC-1998;   98US-0111580.
PR   07-JAN-1999;   99US-0115069.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Rosteck PRJ,  Song HY,  Su EW;
XX
DR   WPI; 2000-431379/37.
DR   N-PSDB; AAA53208.
XX
PT   Novel monkey Fas ligand inhibitor polypeptides, useful for treating
PT   inflammatory or autoimmune disease such as rheumatoid arthritis,
PT   infectious diseases such as chronic hepatitis, and
PT   Ischaemia/Re-perfusion conditions -
XX
PS   Claim 19; Page 91-93; 101pp; English.
XX
CC   The present sequence is the protein sequence of the human Fas ligand
CC   inhibitor (FLINT). The FLINT protein is involved in cell-specific
CC   apoptosis, and can be used to treat inflammatory and autoimmune diseases
CC   such as rheumatoid arthritis, inflammatory bowel disease,
CC   graft-versus-host disease, diabetes, psoriasis and Graves' disease,
CC   infectious diseases such as HIV-induced lymphopenia, fulminant viral
CC   hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated
CC   ulceration, ischaemia and reperfusion conditions including acute
CC   myocardial infarction, acute coronary syndrome, congestive heart failure
CC   and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute lung
CC   injury and acute respiratory distress syndrome, Crohn's disease, brain
CC   trauma and injury, chronic glomerulonephritis, osteoporosis, aplastic
CC   anaemia, myelodysplasia, ulcerative colitis, Down's syndrome, and
CC   multiple sclerosis. In addition, the protein and its gene can be used to
CC   prevent apoptosis following organ transplantation.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 21;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 14
AAY97246
ID   AAY97246 standard; Protein; 300 AA.
XX
AC   AAY97246;
XX
DT   19-DEC-2000  (first entry)
XX
DE   M68 TNF receptor related protein.
XX
KW   M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;
KW   receptor; immune response; cell differentiation; ligand; cancer;
KW   bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
KW   Grave's disease; idiopathic myxodema; autoimmune diabetes;
KW   thrombotic thrombocytopenic purpura; multiple sclerosis;
KW   liver diseases; autoimmune gastritis; ulcerative colitis;
KW   glomerulonephritis; pulmonary fibrosis; heart failure;
KW   atherosclerosis; aplastic anaemia; myelodisplastic syndromes;
KW   osteoporosis; Alzheimers disease; Parkinsons disease; stroke;
KW   myocardial infarction; human.
XX
OS   Homo sapiens.
XX
PN   WO200046247-A1.
XX
PD   10-AUG-2000.
XX
PF   04-FEB-2000; 2000WO-US03037.
XX
PR   05-FEB-1999;   99US-0118902.
PR   20-DEC-1999;   99US-0172754.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Bai C;
XX
DR   WPI; 2000-506066/45.
DR   N-PSDB; AAA53800, AAA53801, AAA53802.
XX
PT   Isolated human M68 nucleic acids and proteins which are part of the
PT   tumor necrosis factor receptor (TNFR) family, useful for identifying
PT   modulators that may be used to treat various diseases e.g. cancer,
PT   osteoporosis, Alzheimer's disease
XX
PS   Claim 1; Page 75-76; 80pp; English.
XX
CC   The M68 protein is a member of a family of proteins which have
CC   roles in immune responses, cell death, cell proliferation and
CC   stimulation of cell differentiation. M68 lacks a transmembrane domain
CC   and is a secreted factor suggesting that it functions as a natural
CC   inhibitor for its ligand. The altered expression pattern of M68 in a
CC   multitude of tissues suggests that M68 may play a role in cancer by
CC   binding to its ligand and blocking apoptotic cell death induced by
CC   such a ligand. This anti-apoptopic role of M68 suggests that
CC   modulators of M68 will be useful in treatment of apoptosis-related
CC   diseases such as various forms of cancer and various bone disorders.
CC   M68 nucleic acids and proteins are therefore useful for treating
CC   conditions involving atypical apoptosis and for identifying
CC   modulators of M68. Modulators of M68 are useful for treatment of
CC   cancer and other diseases associated with abnormal levels of
CC   apoptosis including systemic lupus erythematosus, Hashimoto's
CC   thyroiditis, Grave's disease, idiopathic myxodema, autoimmune
CC   diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,
CC   liver diseases, autoimmune gastritis, ulcerative colitis,
CC   glomerulonephritis, pulmonary fibrosis, heart failure,
CC   atherosclerosis, aplastic anaemia, myelodisplastic syndromes,
CC   osteoporosis, Alzheimers disease, Parkinsons disease, stroke, and
CC   myocardial infarction.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 21;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 15
AAY90357
ID   AAY90357 standard; Protein; 300 AA.
XX
AC   AAY90357;
XX
DT   04-DEC-2000  (first entry)
XX
DE   Human tumour necrosis factor receptor-6 alpha protein sequence.
XX
KW   Human; Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;
KW   ocular neovascularisation; solid tumour; malignancy; prostate cancer;
KW   breast cancer; colon cancer; diabetic retinopathy; microbial infection;
KW   pre-maturity macular degeneration; allergy; inflammation; tissue damage;
KW   thyroid associated opthalmopathy; cell damage; parasitic infection;
KW   bone disease; osteoporosis; atherosclerosis; cardiovascular disease;
KW   neurodegenerative disorder; Alzheimer's disease; immune disorder;
KW   graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma;
KW   psoriasis; septic shock; ulcerative colitis; therapy.
XX
OS   Homo sapiens.
XX
PN   WO200052028-A1.
XX
PD   08-SEP-2000.
XX
PF   03-MAR-2000; 2000WO-US05686.
XX
PR   04-MAR-1999;   99US-0121774.
PR   12-MAR-1999;   99US-0124092.
PR   27-APR-1999;   99US-0131279.
PR   30-APR-1999;   99US-0131964.
PR   02-AUG-1999;   99US-0146371.
PR   01-DEC-1999;   99US-0168235.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Gentz RL,  Ni J,  Ebner R,  Yu G,  Ruben SM,  Feng P;
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XX
DR   WPI; 2000-572174/53.
DR   N-PSDB; AAA37772.
XX
PT   Nucleic acids encoding human tumour necrosis factor receptor (TNFR)
PT   proteins TNFR-6alpha and TNFR-6beta, useful for treating e.g.
PT   Alzheimer's disease, osteoporosis and graft rejection -
XX
PS   Claim 20; Fig 1; 332pp; English.
XX
CC   This sequence represents the human tumour necrosis factor receptor 6
CC   alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA
CC   and protein sequences can be used in the prevention, treatment and
CC   diagnosis of diseases associated with inappropriate TNFR expression. The
CC   nucleic acids, polypeptides, antibodies, agonists and antagonists against
CC   them may be used for the treatment of a range of conditions such as
CC   disorders associated with neovascularisation (especially ocular
CC   neovascularisation) (such as solid tumours and malignancies (e.g.
CC   prostate cancer, breast cancer and colon cancer), diabetic retinopathy
CC   and pre-maturity macular degeneration), allergies, inflammation,
CC   thyroid associated opthalmopathy tissue/cell damage, wounds, microbial
CC   and parasitic infections, bone disease (e.g. osteoporosis),
CC   atherosclerosis, pain, cardiovascular disease (e.g. stroke),
CC   neurodegenerative disorders (e.g. Alzheimer's disease), immune
CC   disorders (e.g. graft rejection), rheumatism, liver disease,
CC   autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative
CC   colitis.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 21;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 16
AAB24395
ID   AAB24395 standard; Protein; 300 AA.
XX
AC   AAB24395;
XX
DT   07-NOV-2000  (first entry)
XX
DE   Human PRO212 protein sequence SEQ ID NO:36.
XX
KW   Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW   diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW   angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW   cytostatic; gene therapy; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO200032221-A2.
XX
PD   08-JUN-2000.
XX
PF   30-NOV-1999;   99WO-US28313.
XX
PR   01-DEC-1998;   98WO-US25108.
PR   16-DEC-1998;   98US-0112850.
PR   12-JAN-1999;   99US-0115554.
PR   08-MAR-1999;   99WO-US05028.
PR   12-MAR-1999;   99US-0123957.
PR   28-APR-1999;   99US-0131445.
PR   14-MAY-1999;   99US-0134287.
PR   02-JUN-1999;   99WO-US12252.
PR   23-JUN-1999;   99US-0141037.
PR   20-JUL-1999;   99US-0144758.
PR   26-JUL-1999;   99US-0145698.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   13-SEP-1999;   99WO-US20944.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   05-OCT-1999;   99WO-US23089.
PR   29-OCT-1999;   99US-0162506.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Ferrara N,  Gerber H,  Hillan KJ,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Klein RD,  Kuo SS,  Paoni NF,  Smith V;
PI   Watanabe CK,  Williams PM,  Wood WI;
XX
DR   WPI; 2000-412154/35.
DR   N-PSDB; AAA77537.
XX
PT   Nucleic acids encoding PRO polypeptides useful for preventing,
PT   diagnosing and treating diagnosing a cardiovascular, endothelial or
PT   angiogenic disorders in mammals -
XX
PS   Claim 72; Fig 16; 315pp; English.
XX
CC   The present invention describes nucleic acids encoding PRO polypeptides
CC   useful for preventing, diagnosing and treating diagnosing a
CC   cardiovascular, endothelial or angiogenic disorder in mammals by
CC   modulating cell proliferation, angiogenesis and cardiovascularisation,
CC   and for identifying agonists and antagonists of these processes. The
CC   nucleic acids and the proteins they encode may be used in the
CC   prevention, treatment and diagnosis of diseases associated with
CC   inappropriate PRO expression such as cardiovascular, endothelial or
CC   angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
CC   cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors
CC   containing them and the PRO polypeptide may be used to treat disorders
CC   associated with decreased PRO expression. AAA77510 to AAA77721 and
CC   AAB24388 to AAB24435 represent nucleotide and protein sequences used in
CC   the exemplification of the present invention.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 21;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
```

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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 17
AAY96596
ID   AAY96596 standard; Protein; 300 AA.
XX
AC   AAY96596;
XX
DT   26-SEP-2000  (first entry)
XX
DE   Human FLINT.
XX
KW   FLINT; osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNFR;
KW   FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
KW   anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
KW   anti-inflammatory; antibacterial; immunosuppressive.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..29
FT                   /label= Signal_peptide
FT   Protein         30..300
FT                   /label= Mature_Protein
XX
PN   WO200037094-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;   99WO-US30734.
XX
PR   22-DEC-1998;   98US-0113407.
PR   30-MAR-1999;   99WO-US06797.
PR   20-OCT-1999;   99US-0172239.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Cohen FJ,  Posada JA,  Wierda D;
XX
DR   WPI; 2000-475441/41.
DR   N-PSDB; AAA51075.
XX
PT   Use of mature FLINT for treating e.g. acute respiratory distress
PT   syndrome, ulcerative colitis or ischemic injury during organ
PT   transplantation
XX
PS   Example 7; Fig 1A-B; 125pp; English.
XX
CC   Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis
CC   factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
CC   prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
CC   mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
CC   treating acute respiratory distress syndrome, treating or inhibiting
CC   ulcerative colitis, inhibiting ischemic injury during organ
CC   transplantation or for organ preservation during transplantation. mFLINT
CC   can also be used to treat acute liver failure, inflammation of the liver,
CC   abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
CC   inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
CC   damage to a cardiac myocyte resulting from abnormal myocardial ischaemia,
CC   Type I diabetes, cancer, damage to an innocent bystander tissue induced
CC   by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
CC   myelodysplastic syndromes and pancytopenic conditions.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 21;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 18
AAE03568
ID   AAE03568 standard; Protein; 300 AA.
XX
AC   AAE03568;
XX
DT   04-AUG-2001  (first entry)
XX
DE   Human native fas ligand inhibitory protein (FLINT).
XX
KW   Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
KW   TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;
KW   acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;
KW   chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;
KW   rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis;
KW   fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;
KW   chronic renal failure; graft-vs-host disease; cutaneous inflammation;
KW   vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;
KW   insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;
KW   Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;
KW   Down's syndrome; multiple sclerosis; cytostatic; nootropic;
KW   neuroprotective; vasotropic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..29
FT                   /label= Signal_peptide
FT   Protein         30..300
FT                   /note= "Mature human FLINT"
FT   Modified-site   203
FT                   /note= "O-linked glycosylation site"
FT   Modified-site   245
FT                   /note= "O-linked glycosylation site"
FT   Cleavage-site   247..248
FT                   /note= "Proteolytic cleavage"
XX
PN   WO200142463-A1.
XX
PD   14-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-US30166.
XX
PR   07-DEC-1999;   99US-0169367.
PR   07-DEC-1999;   99US-0169381.
PR   07-DEC-1999;   99US-0169412.
PR   23-MAR-2000; 2000US-0191430.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
```

```
PI   Lu J,  Witcher DR;
XX
DR   WPI; 2001-381684/40.
XX
PT   New FLINT polypeptide for treating and/or preventing acute lung injury,
PT   acute respiratory distress syndrome, ulcerative colitis, and
PT   graft-versus-host disease, comprises O-linked or N-linked
PT   oligosaccharides -
XX
PS   Example 2; Page 54-55; 60pp; English.
XX
CC   The present sequence is human native fas ligand inhibitory protein
CC   (FLINT). FLINT, a homologue of tumour necrosis factor receptor
CC   protein (TNFR), binds fas ligand (FasL) and thereby preventing the
CC   interaction of FasL with fas. FLINT comprising O-linked or N-linked
CC   oligosaccharides is useful for preventing or treating acute lung injury
CC   (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,
CC   chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),
CC   to facilitate organ preservation for transplantation and to inhibit T
CC   lymphocyte activation. FLINT is useful for treating and/or preventing
CC   diseases such as rheumatoid arthritis, fibroproliferative lung disease,
CC   fibrotic lung disease, acute lung injury, human immunodeficiency virus
CC   (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-
CC   host disease, cutaneous inflammation, vascular leak syndrome,
CC   Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent
CC   diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,
CC   Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as
CC   psoriasis, Down's syndrome, and multiple sclerosis.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 22;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 19
AAB74466
ID   AAB74466 standard; protein; 300 AA.
XX
AC   AAB74466;
XX
DT   30-MAY-2001  (first entry)
XX
DE   Human FLINT native protein.
XX
KW   Human; FLINT; FAS ligand inhibitory protein; analogue; apoptosis;
KW   inflammatory disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 182
FT                   /note= "encoded by ATT"
FT   Misc-difference 243
FT                   /note= "encoded by GCT"
XX
PN   WO200118202-A2.
XX
PD   15-MAR-2001.
XX
PF   31-AUG-2000; 2000WO-US20806.
XX
PR   10-SEP-1999;   99US-0153433.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Atkinson PR,  Tian Y,  Witcher DR;
XX
DR   WPI; 2001-257796/26.
DR   N-PSDB; AAF77696.
XX
PT   Compositions useful for reducing/inducing aggregation of a FLINT analog
PT   comprise a divalent metal cation and a protease-resistant FAS Ligand
PT   Inhibitory Protein (FLINT) analog -
XX
PS   Disclosure; Page 42-43; 44pp; English.
XX
CC   The present invention describes a composition comprising a divalent metal
CC   cation associated with a protease resistant Fas ligand inhibitory protein
CC   (FLINT) analogue. The composition is useful in the treatment of diseases
CC   associated with Fas binding to its ligand, such as acute liver failure,
CC   inflammatory diseases, cerebral ischaemia and apoptosis. The present
CC   sequence is the native FLINT protein.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 22;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 20
AAB71754
ID   AAB71754 standard; Protein; 300 AA.
XX
AC   AAB71754;
XX
DT   02-MAY-2001  (first entry)
XX
DE   Human NTR3.
XX
KW   Human; NTR3; tumour necrosis factor receptor; TNF receptor; anti-HIV;
KW   antianaemic; immunosuppressive; antidiabetic; antiviral; antibacterial;
KW   cytostatic; neuroprotective; antiinflammatory; anorectic; vasotropic;
KW   antirheumatoid; antiarthritic; cerebroprotective; tuberculostatic;
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KW   gene therapy; cancer; blood disorder; brain disorder; autoimmune disease;
KW   infection.
XX
OS   Homo sapiens.
XX
PN   WO200110908-A1.
XX
PD   15-FEB-2001.
XX
PF   02-AUG-2000; 2000WO-US21287.
XX
PR   04-AUG-1999;   99US-0147297.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Hsu H;
XX
DR   WPI; 2001-191521/19.
DR   N-PSDB; AAF62705.
XX
PT   New tumor necrosis factor receptor, NTR3, useful for treating cancers,
PT   stroke, anemia, obesity, rheumatoid arthritis and transplantation
PT   rejection -
XX
PS   Claim 14; Page 129-130; 135pp; English.
XX
CC   The present sequence is the tumour necrosis factor (TNF) receptor
CC   polypeptide NTR3. The NTR3 polynucleotides and polypeptides are useful
CC   for treating diseases such as acquired-immunodeficiency syndrome (AIDS),
CC   anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria,
CC   diabetes mellitus, disseminated intravascular coagulopathy, erythroid
CC   sick syndrome, haemorrhagic shock, hepatitis, insulin resistance,
CC   leprosy, leukaemia, meningitis, multiple sclerosis, myocardial ischaemia,
CC   obesity, rejection of transplanted organs, rheumatoid arthritis, septic
CC   shock syndrome, stroke, adult respiratory distress syndrome (ARDS),
CC   tuberculosis, and a number of viral diseases. The NTR3 polypeptide is
CC   useful for identifying or developing new (ant)agonists of NTR3. It may
CC   be used as an immunogen to which antibodies may be raised. NTR3 nucleic
CC   acid molecules may be useful as hybridisation probes in diagnostic assays
CC   to test, either qualitatively or quantitatively, for the presence of an
CC   NTR3 DNA or corresponding RNA in mammalian tissue or bodily fluid
CC   samples.
XX
SQ   Sequence   300 AA;

  Query Match           100.0%;  Score 1634;  DB 22;  Length 300;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 21
AAB48161
ID   AAB48161 standard; Protein; 300 AA.
XX
AC   AAB48161;
XX
DT   02-APR-2001  (first entry)
XX
DE   Human PRO212 polypeptide.
XX
KW   PRO212; PRO326; PRO1016; neoplastic; cell growth; tumour; cancer;
KW   breast; ovarian; renal; colorectal; uterine; prostate; lung; melanoma;
KW   central nervous system; leukemia; antitumor; cytostatic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..23
FT                   /note= "signal peptide"
FT   Protein         24..300
FT                   /note= "mature protein"
FT   Modified-site   28..37
FT                   /note= "tyrosine kinase phosphorylation site"
FT   Modified-site   63..67
FT                   /note= "cAMP and cGMP-dependant protein kinase
FT                   phosphorylation sites"
FT   Domain          125..145
FT                   /note= "transmembrane domain"
FT   Modified-site   163..167
FT                   /note= "casein kinase II phosphorylation site"
FT   Modified-site   173..177
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   156..162
FT                   /note= "N-myristoylation"
FT   Modified-site   178..184
FT                   /note= "N-myristoylation"
FT   Modified-site   187..191
FT                   /note= "casein kinase II phosphorylation site"
FT   Modified-site   207..213
FT                   /note= "N-myristoylation"
FT   Modified-site   259..263
FT                   /note= "cAMP and cGMP-dependant protein kinase
FT                   phosphorylation sites"
FT   Modified-site   266..272
FT                   /note= "N-myristoylation"
FT   Modified-site   287..293
FT                   /note= "N-myristoylation"
FT   Modified-site   291..295
FT                   /note= "casein kinase II phosphorylation site"
XX
PN   WO200075316-A1.
XX
PD   14-DEC-2000.
XX
PF   20-DEC-1999;   99WO-US30911.
XX
PR   02-JUN-1999;   99WO-US12252.
PR   23-JUN-1999;   99US-0141037.
PR   07-JUL-1999;   99US-0143048.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   30-NOV-1999;   99WO-US28313.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Goddard A,  Gurney AL,  Hillan K,  Napier M,  Wood WI;
XX
DR   WPI; 2001-050025/06.
DR   N-PSDB; AAC84421.
XX
PT   Composition for inhibiting neoplastic cell growth and treating a tumor
PT   or cancer, comprises novel PRO212, PRO326, PRO1016 polypeptides or
PT   agonists of them -
XX
PS   Claim 31; Fig 2; 116pp; English.
XX
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CC   The invention provides PRO212, PRO326 or PRO1016 polypeptides that can be
CC   used for the inhibition of neoplastic cell growth and for treating
CC   tumours. The PRO polypeptides can be expressed by standard recombinant
CC   methodology. The PRO polypeptides or their agonists are useful for
CC   inhibition of neoplastic cell growth and for treating tumours, cancers
CC   such as breast, ovarian, renal, colorectal, uterine, prostate, lung,
CC   bladder or central nervous system cancers or melanoma and leukemia. The
CC   present sequence represents the human PRO212 polypeptide.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 22;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 22
AAB50903
ID   AAB50903 standard; Protein; 300 AA.
XX
AC   AAB50903;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human PRO212 protein.
XX
KW   Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW   antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
KW   antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
KW   antiallergic; antiasthmatic; immune related disorder;
KW   hepatobiliary disease; autoimmune disease; allergy.
XX
OS   Homo sapiens.
XX
PN   WO200073452-A2.
XX
PD   07-DEC-2000.
XX
PF   02-JUN-2000; 2000WO-US15264.
XX
PR   02-JUN-1999;   99WO-US12252.
PR   20-JUL-1999;   99US-0144732.
PR   20-JUL-1999;   99US-0144758.
PR   28-JUL-1999;   99US-0146222.
PR   01-SEP-1999;   99WO-US20111.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   29-OCT-1999;   99US-0162506.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28634.
PR   09-DEC-1999;   99US-0170262.
PR   20-DEC-1999;   99WO-US30911.
PR   05-JAN-2000; 2000WO-US00219.
PR   06-JAN-2000; 2000WO-US00376.
PR   11-FEB-2000; 2000WO-US03565.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   24-FEB-2000; 2000WO-US04914.
PR   15-MAR-2000; 2000WO-US06884.
PR   20-MAR-2000; 2000WO-US07377.
PR   21-MAR-2000; 2000WO-US07532.
PR   30-MAR-2000; 2000WO-US08439.
PR   17-MAY-2000; 2000WO-US13705.
PR   22-MAY-2000; 2000WO-US14042.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Chan B,  Goddard A,  Godowski PJ,  Gurney AL;
PI   Hebert C,  Henzel W,  Kabakoff RC,  Shelton DL,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2001-025253/03.
DR   N-PSDB; AAC91462.
XX
PT   Thirty three nucleic acids encoding PRO polypeptides which are useful
PT   in the diagnosis and treatment of immune related disorders, e.g.
PT   systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
PT   thyroiditis and diabetes mellitus -
XX
PS   Claim 58; Fig 4; 218pp; English.
XX
CC   The present sequence is one of thirty three novel PRO polypeptides.
CC   The PRO polypeptides, anti-PRO antibodies, agonists and
CC   antagonists are useful for treating and diagnosing immune related
CC   disorders such as systemic lupus erythematosus, rheumatoid arthritis,
CC   osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC   systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC   syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC   anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC   immune-mediated renal disease, demyelinating diseases of the central
CC   and peripheral nervous systems (such as multiple sclerosis, idiopathic
CC   demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
CC   inflammatory demyelinating polyneuropathy), hepatobiliary diseases
CC   (such as infectious, autoimmune chronic active hepatitis, primary
CC   biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC   inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC   disease, autoimmune or immune-mediated skin diseases (such as bullous
CC   skin diseases, erythema multiforme, contact dermatitis, psoriasis),
CC   allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC   food hypersensitivity and urticaria), immunological diseases of the
CC   lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
CC   and hypersensitivity pneumonitis), transplantation associated diseases
CC   including graft rejection and graft-versus-host diseases.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 22;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
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```
Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 23
AAE14579
ID   AAE14579 standard; Protein; 300 AA.
XX
AC   AAE14579;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human native FLINT precursor protein.
XX
KW   FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW   organ failure; liver; kidney; pancreas; inflammatory disease;
KW   neutrophil; sepsis; acute respiratory distress syndrome;
KW   acute lung injury; systemic inflammatory response syndrome; SIRS;
KW   multiple organ dysfunction; MODS; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..29
FT                   /label= Leader_peptide
FT   Protein         30..300
FT                   /label= Mature_FLINT
XX
PN   WO200209668-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-US21105.
XX
PR   02-AUG-2000; 2000US-222476P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Witcher DR;
XX
DR   WPI; 2002-206149/26.
XX
PT   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT   useful for treating e.g. sepsis or respiratory distress syndrome,
PT   involves pulmonary administration of a therapeutic amount of the FLINT
PT   or FLINT analog -
XX
PS   Disclosure; Page 31-32; 35pp; English.
XX
CC   The invention relates to a new method of administering FLINT
CC   (FAS ligand inhibitory protein) or FLINT analog that involves pulmonary
CC   administration of a therapeutic amount of the FLINT or FLINT analog.
CC   The method enables systemic absorption of FLINT through lungs and
CC   significantly reduces or eliminates the need for administering FLINT by
CC   injection or other routes of administration. The method is useful in
CC   treating disorders related to enhanced apoptosis (e.g. organ failure
CC   in liver, kidneys and pancreas) and inflammatory diseases associated with
CC   neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC   acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC   multiple organ dysfunction (MODS)). The method minimises the pain
CC   and discomfort of injection methods. The present sequence is human
CC   native FLINT precursor protein.
XX
SQ   Sequence   300 AA;

  Query Match           100.0%;  Score 1634;  DB 23;  Length 300;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 24
AAE20848
ID   AAE20848 standard; Protein; 300 AA.
XX
AC   AAE20848;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human tumour necrosis factor receptor (TNFR)-6alpha protein.
XX
KW   Human; tumour necrosis factor receptor; TNFR-6alpha; TNFR-6beta; therapy;
KW   immune system-related disorder; inflammatory disease; immunosuppressive;
KW   bowel disease; encephalitis; atherosclerosis; gastrointestinal-Gen;
KW   autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
KW   multiple sclerosis; Crohn's disease; autoimmune encephalitis; allergy;
KW   graft versus host disease; GVHD; antiinflammatory; psoriasis; arthritis;
KW   neuroprotective; antiarteriosclerotic; dermatological; asthma; receptor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..30
FT                   /label= Signal_peptide
FT   Protein         31..300
FT                   /note= "Human TNFR-6alpha protein"
FT   Domain          31..283
FT                   /note= "Extracellular domain"
FT   Region          31..46
FT                   /note= "Antigenic region"
FT   Region          57..117
FT                   /note= "Antigenic region"
FT   Region          132..175
FT                   /note= "Antigenic region"
FT   Region          185..194
FT                   /note= "Antigenic region"
FT   Region          205..217
FT                   /note= "Antigenic region"
FT   Region          239..264
FT                   /note= "Antigenic region"
FT   Region          283..298
FT                   /note= "Antigenic region"
XX
PN   WO200218622-A2.
XX
PD   07-MAR-2002.
XX
PF   24-AUG-2001; 2001WO-US26396.
XX
PR   25-AUG-2000; 2000US-227598P.
PR   21-NOV-2000; 2000US-252131P.
PR   06-JUL-2001; 2001US-303224P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
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```
PI   Gentz RL,  Ebner R,  Yu G,  Ruben SM,  Ni J,  Feng P;
XX
DR   WPI; 2002-281068/32.
DR   N-PSDB; AAD33281.
XX
PT   Novel nucleic acid molecules comprising a polynucleotide encoding human
PT   tumor necrosis factor receptor (TNFR)-6alpha and 6beta polypeptides
PT   useful for treating disease e.g. inflammatory and autoimmune disorders
PT   -
XX
PS   Claim 1; Fig 1; 350pp; English.
XX
CC   The invention relates to human tumour necrosis factor receptor (TNFR)-
CC   6alpha and 6beta protein and their corresponding nucleic acids. The
CC   invention provides screening methods for identifying agonists and
CC   antagonists of TNFR-6alpha and 6beta activity. The invention also
CC   provides diagnostic and therapeutic methods for detecting and treating
CC   immune system-related disorders. The method is useful for treating or
CC   preventing an inflammatory disease or disorder selected from bowel
CC   disease, encephalitis, atherosclerosis and psoriasis, an autoimmune
CC   disease or disorder selected from systemic lupus erythematosus,
CC   arthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease,
CC   and autoimmune encephalitis, graft versus host disease (GVHD), and an
CC   allergy or asthma. The present sequence is human TNFR-6alpha protein.
XX
SQ   Sequence   300 AA;

  Query Match             100.0%;  Score 1634;  DB 23;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 25
AAG73740
ID   AAG73740 standard; Protein; 341 AA.
XX
AC   AAG73740;
XX
DT   03-SEP-2001  (first entry)
XX
DE   Human colon cancer antigen protein SEQ ID NO:4504.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   colorectal carcinoma; chromosome 20.
XX
OS   Homo sapiens.
XX
PN   WO200122920-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-US26524.
XX
PR   29-SEP-1999;   99US-0157137.
PR   03-NOV-1999;   99US-0163280.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Barash SC,  Birse CE,  Rosen CA;
XX
DR   WPI; 2001-235357/24.
DR   N-PSDB; AAH33171.
XX
PT   Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT   useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS   Claim 11; Page 6304-6306; 9803pp; English.
XX
CC   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC   cancer-associated nucleic acid molecules (N) and proteins (P), where
CC   the proteins are collectively known as colon cancer antigens. The colon
CC   cancer antigens have cytostatic activity and can be used in gene
CC   therapy and vaccine production. N and P may be used in the prevention,
CC   diagnosis and treatment of diseases associated with inappropriate P
CC   expression. For example, N and P may be used to treat disorders
CC   associated with decreased expression by rectifying mutations or deletions
CC   in a patient's genome that affect the activity of P by expressing
CC   inactive proteins or to supplement the patients own production of P.
CC   Additionally, N may be used to produce the colon cancer-associated Ps,
CC   by inserting the nucleic acids into a host cell and culturing the cell
CC   to express the proteins. N and P can be used in the prevention, diagnosis
CC   and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC   and AAB77789 represent sequences used in the exemplification of the
CC   present invention.
CC   N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC   missing at time of publication, meaning no sequences are present for
CC   SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ   Sequence   341 AA;

  Query Match             100.0%;  Score 1634;  DB 22;  Length 341;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-121;
  Matches  300;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         42 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 101

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 161

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 221

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 281

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 341


RESULT 26
AAY77458
ID   AAY77458 standard; Protein; 300 AA.
XX
AC   AAY77458;
XX
DT   05-JUN-2000  (first entry)
XX
DE   Human TNF receptor-like protein, HDTEA84.
XX
KW   TNF receptor family; tumour necrosis factor; HDTEA84; HSLJD37R;
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KW   Rank-like protein; RANKL; immune disorder; inflammation; allergy;
KW   immunosuppressant; antiarthritic; antirheumatoid; antiinflammatory;
KW   dermatological; antithyroid.
XX
OS   Homo sapiens.
XX
PN   WO200001817-A2.
XX
PD   13-JAN-2000.
XX
PF   06-JUL-1999;   99WO-US12366.
XX
PR   06-JUL-1998;   98US-0110938.
PR   13-JUL-1998;   98US-0114466.
PR   23-JUL-1998;   98US-0093897.
PR   12-AUG-1998;   98US-0132968.
PR   18-AUG-1998;   98US-0136214.
PR   11-SEP-1998;   98US-0099999.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Bates EEM,  Lebecque SJE,  Murphy EE,  Mattson JD,  Gorman DM;
PI   Hedrick JA,  Wang L,  Zlotnik A,  Murgolo NJ,  Greene JR,  Johnston JA;
PI   Bazan JF,  Mahony D,  Lees EM;
XX
DR   WPI; 2000-171015/15.
DR   N-PSDB; AAZ92404.
XX
PT   New isolated mammalian genes, used to develop products for treating
PT   e.g. immune, inflammatory or allergic abnormalities, cancers or
PT   degenerative conditions  -
XX
PS   Claim 24; Page 157; 218pp; English.
XX
CC   The invention relates to a number of primate and/or rodent proteins, and
CC   the genes which encode them. The invention encompasses human dendritic
CC   cell prostaglandin transporter (DC-PGT); the TNF (tumour necrosis
CC   factor) receptor family-related proteins HDTEA84, HSLJD37R and RANKL;
CC   human CC chemokine HCC5; human deubiquitinating proteins Dub11 and Dub
CC   12; human MD-1 and human and murine MD-2 proteins, which exhibit the
CC   properties of ligands for proteins comprising a leucine-rich motif
CC   (LRR); human cyclin E2; cDNAs encoding these proteins; and antibodies
CC   against these proteins. The proteins can be used for modulating the
CC   physiology or development of a cell. They can be used to mediate uptake
CC   of substrates (e.g., prostaglandin-like molecules), to modulate or
CC   mediate cellular interactions (e.g., induce or prevent trafficking,
CC   proliferation, or differentiation of cells), or are intracellular
CC   proteins which are important in various cellular processes such as the
CC   deubiquitination of proteins or cell cycle regulation. The products can
CC   be used for treating medical conditions such as immune, inflammatory or
CC   allergic disorders, or abnormal cellular proliferation, for example,
CC   cancers or degenerative conditions. They can be used to modulate immune
CC   responses in disease states e.g., autoimmune disorders, including
CC   rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's
CC   autoimmune thyroiditis, as well as acute and chronic inflammatory
CC   responses in which T cell activation, expansion, and/or immunological T
CC   cell memory play an important role. Sequences AAY77458-Y77461 and
CC   AAY77465-Y77468 represent TNF receptor family-related proteins. AAY77458
CC   is the human protein HDTEA84, AAY77459-Y77461 are human HSLJD37R
CC   proteins, AAY77465 is murine Rank-like protein RANKL, and AAY77466-Y77468
CC   are human RANKL proteins.
XX
SQ   Sequence   300 AA;

  Query Match           99.1%;  Score 1620;  DB 21;  Length 300;
  Best Local Similarity  99.3%;  Pred. No. 1.8e-120;
  Matches  298;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              |||||||  |||||||||||||||||||||  ||||||||||||||||||||||||||||
Db         61 PCRRDSPMTCGPCPPRHYTQFWNYLERCRYCYVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 27
AAB19710
ID   AAB19710 standard; Protein; 300 AA.
XX
AC   AAB19710;
XX
DT   05-FEB-2001  (first entry)
XX
DE   Human FAS ligand inhibitor protein FLINT native sequence.
XX
KW   FLINT; FAS ligand inhibitory protein; human; protease resistant;
KW   acute lung injury; acute respiratory distress syndrome;
KW   chronic obstructive pulmonary disease; pulmonary fibrosis;
KW   ulcerative colitis; therapy; organ transplantation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..29
FT                   /label= Signal_peptide
FT   Protein         30..300
FT                   /label= Mature_protease
FT   Cleavage-site   247..248
FT                   /note= "cleaved by trypsin-like proteases"
XX
PN   WO200058466-A2.
XX
PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-US06418.
XX
PR   30-MAR-1999;   99US-0126839.
PR   21-JUN-1999;   99US-0140073.
PR   04-AUG-1999;   99US-0147071.
PR   20-OCT-1999;   99US-0160524.
PR   21-OCT-1999;   99US-0160669.
PR   20-DEC-1999;   99US-0172744.
PR   26-JAN-2000; 2000US-0178184.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Rathnachalam R,  Witcher DR;
XX
DR   WPI; 2000-664925/64.
DR   N-PSDB; AAA88731.
XX
PT   Novel protease resistant FAS ligand inhibitory protein analogues
PT   resistant to in vivo or in vitro proteolysis at amino acid position 218
PT   of the mature protein, useful for treating autoimmune diseases  -
XX
PS   Disclosure; Page 97-98; 100pp; English.
XX
CC   The present sequence is that of human FAS ligand inhibitory protein
CC   FLINT native protein.  FLINT is a tumour necrosis factor receptor
CC   homologue that binds FAS ligand, preventing its interaction with
CC   FAS.  This interaction is implicated in runaway apoptosis and
CC   inflammatory disease.  FLINT also binds to LIGHT, a membrane-bound
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CC   ligand, which may play a role in immune modulation and apoptosis.
CC   The invention relates to novel FLINT analogues (see also AAB19706-09)
CC   that are resistant to proteolysis by trypsin-like proteases between
CC   positions 218 and 219 of the FLINT mature protein sequence (see
CC   AAB19705), equivalent to positions 247 and 248 of the present
CC   sequence. The analogues have amino acid substitutions in the
CC   region comprising amino acids 214-222, and optionally at residues
CC   34, 36, 132, 194 and/or 196, of the mature protein. Nucleic acids,
CC   vectors and transformed host cells for recombinant production of
CC   the analogues are claimed. FLINT cDNA (see AAA88731) is used as a
CC   template for introducing the required point mutations. The
CC   protease resistant FLINT analogues are used to prevent or treat
CC   acute lung injury, acute respiratory stress syndrome, ulcerative
CC   colitis, chronic obstructive pulmonary disease, pulmonary
CC   fibrosis, to inhibit T lymphocyte activation, and to facilitate
CC   organ preservation for transplantation (claimed).
XX
SQ   Sequence   300 AA;

  Query Match             99.1%;  Score 1619;  DB 21;  Length 300;
  Best Local Similarity   99.3%;  Pred. No. 2.2e-120;
  Matches  298;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LIVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWAPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 28
AAY96597
ID   AAY96597 standard; Protein; 300 AA.
XX
AC   AAY96597;
XX
DT   26-SEP-2000  (first entry)
XX
DE   Human FLINT.
XX
KW   FLINT; osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNFR;
KW   FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
KW   anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
KW   anti-inflammatory; antibacterial; immunosuppressive.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..29
FT                   /label= Signal_peptide
FT   Protein         30..300
FT                   /label= Mature_Protein
XX
PN   WO200037094-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;   99WO-US30734.
XX
PR   22-DEC-1998;   98US-0113407.
PR   30-MAR-1999;   99WO-US06797.
PR   20-OCT-1999;   99US-0172239.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Cohen FJ,  Posada JA,  Wierda D;
XX
DR   WPI; 2000-475441/41.
DR   N-PSDB; AAA51076.
XX
PT   Use of mature FLINT for treating e.g. acute respiratory distress
PT   syndrome, ulcerative colitis or ischemic injury during organ
PT   transplantation
XX
PS   Example 1; Fig 2A-B; 125pp; English.
XX
CC   Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis
CC   factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
CC   prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
CC   mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
CC   treating acute respiratory distress syndrome, treating or inhibiting
CC   ulcerative colitis, inhibiting ischemic injury during organ
CC   transplantation or for organ preservation during transplantation. mFLINT
CC   can also be used to treat acute liver failure, inflammation of the liver,
CC   abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
CC   inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
CC   damage to a cardiac myocyte resulting from abnormal myocardial ischaemia,
CC   Type I diabetes, cancer, damage to an innocent bystander tissue induced
CC   by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
CC   myelodysplastic syndromes and pancytopenic conditions.
XX
SQ   Sequence   300 AA;

  Query Match             99.1%;  Score 1619;  DB 21;  Length 300;
  Best Local Similarity   99.3%;  Pred. No. 2.2e-120;
  Matches  298;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LIVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWAPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 29
AAE03570
ID   AAE03570 standard; Protein; 300 AA.
XX
AC   AAE03570;
XX
DT   04-AUG-2001  (first entry)
XX
DE   Human fas ligand inhibitory protein (FLINT).
XX
KW   Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
KW   TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;
KW   acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;
KW   chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;
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```
KW   rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis;
KW   fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;
KW   chronic renal failure; graft-vs-host disease; cutaneous inflammation;
KW   vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;
KW   insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;
KW   Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;
KW   Down's syndrome; multiple sclerosis; cytostatic; nootropic;
KW   neuroprotective; vasotropic.
XX
OS   Homo sapiens.
XX
PN   WO200142463-A1.
XX
PD   14-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-US30166.
XX
PR   07-DEC-1999;   99US-0169367.
PR   07-DEC-1999;   99US-0169381.
PR   07-DEC-1999;   99US-0169412.
PR   23-MAR-2000; 2000US-0191430.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Lu J,  Witcher DR;
XX
DR   WPI; 2001-381684/40.
DR   N-PSDB; AAD07385.
XX
PT   New FLINT polypeptide for treating and/or preventing acute lung injury,
PT   acute respiratory distress syndrome, ulcerative colitis, and
PT   graft-versus-host disease, comprises O-linked or N-linked
PT   oligosaccharides -
XX
PS   Disclosure; Page 56-57; 60pp; English.
XX
CC   The present sequence is human fas ligand inhibitory protein
CC   (FLINT). FLINT, a homologue of tumour necrosis factor receptor
CC   protein (TNFR), binds fas ligand (FasL) and thereby preventing the
CC   interaction of FasL with fas. FLINT comprising O-linked or N-linked
CC   oligosaccharides is useful for preventing or treating acute lung injury
CC   (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,
CC   chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),
CC   to facilitate organ preservation for transplantation and to inhibit T
CC   lymphocyte activation. FLINT is useful for treating and/or preventing
CC   diseases such as rheumatoid arthritis, fibroproliferative lung disease,
CC   fibrotic lung disease, acute lung injury, human immunodeficiency virus
CC   (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-
CC   host disease, cutaneous inflammation, vascular leak syndrome,
CC   Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent
CC   diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,
CC   Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as
CC   psoriasis, Down's syndrome, and multiple sclerosis.
XX
SQ   Sequence   300 AA;

  Query Match            99.1%;  Score 1619;  DB 22;  Length 300;
  Best Local Similarity  99.3%;  Pred. No. 2.2e-120;
  Matches  298;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LIVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWAPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 30
AAB83950
ID   AAB83950 standard; Protein; 300 AA.
XX
AC   AAB83950;
XX
DT   06-AUG-2001  (first entry)
XX
DE   Amino acid sequence of a human FLINT polypeptide.
XX
KW   Human; FLINT; FAS ligand inhibitory protein; lung disease;
KW   lung disorder; chronic obstructive pulmonary disease; pulmonary fibrosis;
KW   T-cell activation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..29
FT                   /note= "signal peptide"
FT   Protein         30..300
FT                   /note= "mature protein"
XX
PN   WO200128582-A2.
XX
PD   26-APR-2001.
XX
PF   06-OCT-2000; 2000WO-US26241.
XX
PR   20-OCT-1999;   99US-0160613.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Bumol TF,  Cohen FJ;
XX
DR   WPI; 2001-290820/30.
DR   N-PSDB; AAF89920.
XX
PT   New FAS Ligand Inhibitory protein (FLINT) for use as a medicament in
PT   treating and/or inhibiting lung disease and inhibiting T-cell
PT   proliferation  -
XX
PS   Disclosure; Page 36-37; 37pp; English.
XX
CC   The present sequence represents a human FLINT (FAS Ligand Inhibitory
CC   Protein). FLINT polypeptides are capable of disrupting the Fas
CC   ligand-Fas receptor interactions. The FLINT protein is useful the
CC   treatment and inhibition of lung disease and lung disorders. FLINT
CC   is useful for treating and inhibiting chronic obstructive pulmonary
CC   disease and pulmonary fibrosis and inhibiting T-cell activation and
CC   proliferation.
XX
SQ   Sequence   300 AA;

  Query Match            99.1%;  Score 1619;  DB 22;  Length 300;
  Best Local Similarity  99.3%;  Pred. No. 2.2e-120;
  Matches  298;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
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Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LIVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWAPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 31
AAB68045
ID   AAB68045 standard; Protein; 300 AA.
XX
AC   AAB68045;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Amino acid sequence of a human FLINT polypeptide.
XX
KW   FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;
KW   Fas ligand; acute liver failure; cerebral ischemia; apoptosis.
XX
OS   Homo sapiens.
XX
PN   WO200118055-A1.
XX
PD   15-MAR-2001.
XX
PF   31-AUG-2000; 2000WO-US20807.
XX
PR   10-SEP-1999;   99US-0153339.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Atkinson PR,  Tian Y,  Witcher DR;
XX
DR   WPI; 2001-273382/28.
DR   N-PSDB; AAF84738.
XX
PT   Compositions comprising a divalent metal cation and a FAS Ligand
PT   Inhibitory Protein (FLINT), for reducing or inducing aggregation of
PT   FLINT and for treating diseases involving FasL/Fas and/or
PT   LIGHT/LT-beta-R receptor interactions
XX
PS   Disclosure; Page 41-42; 44pp; English.
XX
CC   The present sequence represents a human FLINT (FAS Ligand Inhibitory
CC   Protein) polypeptide. The specification describers a composition
CC   comprising a divalent metal cation and FLINT protein. The composition
CC   is used either for reducing, reversing or eliminating aggregation and
CC   precipitation of FLINT or for inducing oligomerisation or aggregation
CC   of FLINT molecules. They can be used for purifying FLINT and/or
CC   maintaining FLINT in solution. The compositions are used to treat
CC   and/or prevent disorders associated with the binding of Fas to FasL
CC   and/or LIGHT to the LTbetaR and/or TR2/HVEM receptors. Uses include the
CC   treatment of acute liver failure and cerebral ischemia and the prevention
CC   of apoptosis.
XX
SQ   Sequence   300 AA;

  Query Match             99.1%;  Score 1619;  DB 22;  Length 300;
  Best Local Similarity   99.3%;  Pred. No. 2.2e-120;
  Matches  298;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LIVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWAPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300


RESULT 32
AAB68048
ID   AAB68048 standard; Protein; 300 AA.
XX
AC   AAB68048;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Amino acid sequence of a human FLINT polypeptide.
XX
KW   FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;
KW   Fas ligand; acute liver failure; cerebral ischemia; apoptosis.
XX
OS   Homo sapiens.
XX
PN   WO200118041-A2.
XX
PD   15-MAR-2001.
XX
PF   31-AUG-2000; 2000WO-US20805.
XX
PR   10-SEP-1999;   99US-0153445.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Atkinson PR,  Tian Y,  Witcher DR;
XX
DR   WPI; 2001-273381/28.
DR   N-PSDB; AAF84739.
XX
PT   Compositions comprising a divalent metal cation and a FAS Ligand
PT   Inhibitory Protein (FLINT), for reducing or inducing aggregation of
PT   FLINT and for treating diseases involving FasL/Fas and/or
PT   LIGHT/LT-beta-R receptor interactions
XX
PS   Disclosure; Page 32-33; 33pp; English.
XX
CC   The present sequence represents a human FLINT (FAS Ligand Inhibitory
CC   Protein) polypeptide. The specification describers a composition
CC   comprising a divalent metal cation and FLINT protein. The composition
CC   is used either for reducing, reversing or eliminating aggregation and
CC   precipitation of FLINT or for inducing oligomerisation or aggregation
CC   of FLINT molecules. They can be used for purifying FLINT and/or
CC   maintaining FLINT in solution. The compositions are used to treat
CC   and/or prevent disorders associated with the binding of Fas to FasL
CC   and/or LIGHT to the LTbetaR and/or TR2/HVEM receptors. Uses include the
CC   treatment of acute liver failure and cerebral ischemia and the prevention
CC   of apoptosis.
XX
SQ   Sequence   300 AA;

  Query Match             99.1%;  Score 1619;  DB 22;  Length 300;
  Best Local Similarity   99.3%;  Pred. No. 2.2e-120;
  Matches  298;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LIVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWAPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
```

RESULT 33
AAE14580
ID AAE14580 standard; Protein; 300 AA.
XX
AC AAE14580;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human FLINT analog.
XX
KW FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW organ failure; liver; kidney; pancreas; inflammatory disease;
KW neutrophil; sepsis; acute respiratory distress syndrome;
KW acute lung injury; systemic inflammatory response syndrome; SIRS;
KW multiple organ dysfunction; MODS; human.
XX
OS Homo sapiens.
XX
PN WO200209668-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-US21105.
XX
PR 02-AUG-2000; 2000US-222476P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Micanovic R, Witcher DR;
XX
DR WPI; 2002-206149/26.
DR N-PSDB; AAD27869.
XX
PT Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT useful for treating e.g. sepsis or respiratory distress syndrome,
PT involves pulmonary administration of a therapeutic amount of the FLINT
PT or FLINT analog -
XX
PS Disclosure; Page 34-35; 35pp; English.
XX
CC The invention relates to a new method of administering FLINT
CC (FAS ligand inhibitory protein) or FLINT analog that involves pulmonary
CC administration of a therapeutic amount of the FLINT or FLINT analog.
CC The method enables systemic absorption of FLINT through lungs and
CC significantly reduces or eliminates the need for administering FLINT by
CC injection or other routes of administration. The method is useful in
CC treating disorders related to enhanced apoptosis (e.g. organ failure
CC in liver, kidneys and pancreas) and inflammatory diseases associated with
CC neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC multiple organ dysfunction (MODS)). The method minimises the pain
CC and discomfort of injection methods. The present sequence is human
CC FLINT analog.
XX

SQ Sequence 300 AA;

Query Match 99.1%; Score 1619; DB 23; Length 300;
Best Local Similarity 99.3%; Pred. No. 2.2e-120;
Matches 298; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LIVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GWAPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
```

RESULT 34
AAY42183
ID AAY42183 standard; Protein; 302 AA.
XX
AC AAY42183;
XX
DT 17-DEC-1999 (first entry)
XX
DE Human FLINT #2 protein sequence.
XX
KW Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
KW apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW reperfusion-associated injury; aplastic anaemia; differentiation;
KW growth; myelodysplastic syndrome; pancytopenic condition;
KW myocardial ischaemia.
XX
OS Homo sapiens.
XX
PN WO9950413-A2.
XX
PD 07-OCT-1999.
XX
PF 30-MAR-1999; 99WO-US06797.
XX
PR 30-MAR-1998; 98US-0079856.
PR 20-MAY-1998; 98US-0086074.
PR 09-SEP-1998; 98US-0099643.
PR 17-DEC-1998; 98US-0112577.
PR 18-DEC-1998; 98US-0112703.
PR 18-DEC-1998; 98US-0112933.
PR 22-DEC-1998; 98US-0113407.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Bumol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;
PI Hui KY, Kharitonenkov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;
PI Song HY, Wang J, Wu X, Zuckerman SH;
XX
DR WPI; 1999-591319/50.
DR N-PSDB; AAZ25376.
XX
PT Use of mature FLINT for treating acute liver failure, inflammation,
PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic
PT and proinflammatory activity
XX

```
PS   Example 2; Fig 2; 99pp; English.
XX
CC   The present invention describes therapeutic applications of mature FLINT
CC   (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
CC   (mFLINT), which is a member of the tumour necrosis factor receptor
CC   superfamily, is used for treating acute liver failure, inflammation of
CC   the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
CC   with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
CC   injury or disorder such as hypercoagulation (including use with
CC   thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
CC   or disorder, Type I diabetes, cancer, cell damage or damage to an
CC   innocent bystander tissue that is induced by a chemotherapeutic agent or
CC   therapeutic irradiation, treating haematopoietic progenitor cells that
CC   have been exposed to therapeutic radiation or chemotherapy, aplastic
CC   anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
CC   also used for promoting the growth or differentiation of a haematopoietic
CC   progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
CC   resulting from abnormal myocardial ischaemia. The present sequence
CC   represents human FLINT.
XX
SQ   Sequence   302 AA;

  Query Match             98.5%;  Score 1610;  DB 20;  Length 302;
  Best Local Similarity   98.7%;  Pred. No. 1.1e-119;
  Matches  298;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    1;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRA--CRCRTG 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRCRTG 120

Qy        119 FFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALG 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALG 180

Qy        179 LALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEA 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LALNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEA 240

Qy        239 PEGWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLP 298
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PEGWAPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLP 300

Qy        299 VH 300
               |
Db        301 WH 302


RESULT 35
ABP41980
ID   ABP41980 standard; Protein; 326 AA.
XX
AC   ABP41980;
XX
DT   22-AUG-2002  (first entry)
XX
DE   Human ovarian antigen HTPCH84, SEQ ID NO:3112.
XX
KW   Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW   ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW   infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW   PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW   inflammatory condition; immune disorder; blood disorder;
KW   cardiovascular disorder; respiratory disorder; neurological disorder;
KW   gastrointestinal disorder; urinary system disorder; drug screening;
KW   gene therapy; chromosome mapping; forensic analysis;
KW   antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW   antiinflammatory; gynaecological; reproductive.
XX
OS   Homo sapiens.
XX
PN   WO200200677-A1.
XX
PD   03-JAN-2002.
XX
PF   07-JUN-2001; 2001WO-US18569.
XX
PR   07-JUN-2000; 2000US-209467P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Birse CE,  Rosen CA;
XX
DR   WPI; 2002-147878/19.
DR   N-PSDB; ABQ55057.
XX
PT   Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT   useful in the prevention, treatment and diagnosis of cancer (e.g.
PT   ovarian cancer), immune disorders, cardiovascular disorders and
PT   neurological diseases -
XX
PS   Claim 11; SEQ ID No 3112; 2922pp; English.
XX
CC   The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC   ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC   encompasses polypeptides 90% identical and polynucleotides 95% identical
CC   to the sequences of the invention. The invention additionally relates to
CC   recombinant vectors and host cells comprising human ovarian antigen
CC   polynucleotides, antibodies against human ovarian antigens, and the use
CC   of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC   treating, prognosing or preventing various ovary and/or breast-related
CC   disorders. Such conditions include ovarian cancer and breast cancer, and
CC   metastatic tumours of ovarian or breast origin, reproductive system
CC   disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC   polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC   disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC   shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC   vaginitis), immune disorders (e.g., congenital and acquired
CC   immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC   blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC   respiratory disorders, neurological disorders, gastrointestinal disorders
CC   and urinary system disorders. Ovarian antigen polypeptides and
CC   polynucleotides may also be used in screening for compounds which
CC   modulate ovarian antigen expression or activity. The polynucleotides may
CC   further be used for gene therapy, chromosome mapping, in the
CC   identification of individuals and in forensic analysis, and the
CC   polypeptides may be used as food additives or to prepare antibodies
CC   useful in disease diagnosis, drug targeting and phenotyping. The present
CC   sequence represents a human ovarian antigen of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   326 AA;

  Query Match             93.8%;  Score 1532;  DB 23;  Length 326;
  Best Local Similarity   99.6%;  Pred. No. 1.8e-113;
  Matches  280;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 94

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 154

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 214

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        215 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 274

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALR 281
              |||||||||||||||||||||||||||||||||||||||| |
Db        275 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQAAR 315


RESULT 36
AAB03623
ID   AAB03623 standard; Protein; 300 AA.
XX
AC   AAB03623;
XX
DT   03-JAN-2001  (first entry)
XX
DE   Human Fas ligand inhibitor FLINT mutant.
XX
KW   Human; Fas ligand inhibitor; FLINT; apoptosis; autoimmune disease;
KW   inflammation; infectious disease; ischaemia; Alzheimer's disease;
KW   Parkinson's disease; Crohn's disease; transplantation; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..29
FT                   /label= signal_peptide
FT   Domain          1..42
FT                   /label= domain_1
FT   Misc-difference 10
FT                   /note= "wild-type Ser substituted by Leu"
FT   Misc-difference 16
FT                   /note= "wild-type Leu substituted by Trp"
FT   Misc-difference 23
FT                   /note= "wild-type Pro substituted by Leu"
FT   Misc-difference 27
FT                   /note= "wild-type Val is substituted by Met"
FT   Misc-difference 30
FT                   /note= "wild-type Val substituted by Ala"
FT   Misc-difference 31
FT                   /note= "wild-type Ala substituted by Thr"
FT   Misc-difference 33
FT                   /note= "wild-type Thr substituted by Ala"
FT   Misc-difference 41
FT                   /note= "wild-type Ala substituted by Thr"
FT   Misc-difference 42
FT                   /note= "wild-type Glu substituted by Asp"
FT   Domain          43..85
FT                   /label= domain_2
FT   Misc-difference 46
FT                   /note= "wild-type Arg substituted by Trp"
FT   Misc-difference 60
FT                   /note= "wild-type Arg substituted by Gln"
FT   Domain          86..122
FT                   /label= domain_3
FT   Misc-difference 104
FT                   /note= "wild-type Ala substituted by Pro"
FT   Domain          123..165
FT                   /label= domain_4
FT   Misc-difference 131
FT                   /note= "wild-type Ser substituted by Leu"
FT   Misc-difference 136
FT                   /note= "wild-type Ala substituted by Thr"
FT   Misc-difference 139
FT                   /note= "wild-type Ile substituted by Met"
FT   Misc-difference 191
FT                   /note= "wild-type Thr substituted by Ala"
FT   Misc-difference 198
FT                   /note= "wild-type Gly substituted by Ala"
FT   Misc-difference 208
FT                   /note= "wild-type Ala substituted by Thr"
FT   Misc-difference 212
FT                   /note= "wild-type Glu substituted by Lys"
FT   Misc-difference 238
FT                   /note= "wild-type Ala substituted by Thr"
FT   Misc-difference 254
FT                   /note= "wild-type Gln substituted by Arg"
FT   Misc-difference 258
FT                   /note= "wild-type Arg substituted by Gln"
FT   Misc-difference 259
FT                   /note= "wild-type Arg substituted by Gln"
FT   Misc-difference 266
FT                   /note= "wild-type Gly substituted by Glu"
FT   Misc-difference 299
FT                   /note= "wild-type Val substituted by Gly"
XX
PN   WO200034782-A1.
XX
PD   15-JUN-2000.
XX
PF   07-DEC-1999;   99WO-US28696.
XX
PR   09-DEC-1998;   98US-0111575.
PR   09-DEC-1998;   98US-0111580.
PR   07-JAN-1999;   99US-0115069.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Rosteck PRJ,  Song HY,  Su EW;
XX
DR   WPI; 2000-431379/37.
XX
PT   Novel monkey Fas ligand inhibitor polypeptides, useful for treating
PT   inflammatory or autoimmune disease such as rheumatoid arthritis,
PT   infectious diseases such as chronic hepatitis, and
PT   Ischaemia/Re-perfusion conditions -
XX
PS   Claim 19; Page -; 101pp; English.
XX
CC   The present sequence is a mutant protein sequence of the human Fas
CC   ligand inhibitor (FLINT). The FLINT protein is involved in cell-specific
CC   apoptosis, and can be used to treat inflammatory and autoimmune diseases
CC   such as rheumatoid arthritis, inflammatory bowel disease,
CC   graft-versus-host disease, diabetes, psoriasis and Graves' disease,
CC   infectious diseases such as HIV-induced lymphopenia, fulminant viral
CC   hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated
CC   ulceration, ischaemia and reperfusion conditions including acute
CC   myocardial infarction, acute coronary syndrome, congestive heart failure
CC   and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute
CC   lung injury and acute respiratory distress syndrome, Crohn's disease,
CC   brain trauma and injury, chronic glomerulonephritis, osteoporosis,
CC   aplastic anaemia, myelodysplasia, ulcerative colitis, Down's syndrome,
CC   and multiple sclerosis. In addition, the protein and its gene can be used
CC   to prevent apoptosis following organ transplantation.
CC   Note: The present sequence is not shown in the specification but is
CC   derived from the Homo sapiens wild-type FLINT sequence shown on page
CC   91-93 (AAB03621).
XX
SQ   Sequence   300 AA;

  Query Match             92.4%;  Score 1509;  DB 21;  Length 300;
  Best Local Similarity   91.7%;  Pred. No. 1.1e-111;
  Matches  275;  Conservative    8;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||| ||||| |||||| |||:||  | ||||||| :||| |||||||||||||:
Db          1 MRALEGPGLLLLCLVWALPALLLVPAMRGATEAPTYPWRDTDTGEWLVCAQCPPGTFVQQ 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARPCHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              |||||||||| |||| ||:|||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHALCPPGTGVMAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
```

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Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              |||||||||| |||||| ||||||||| |||:||||||||||||||||||||||||| ||
Db        181 LNVPGSSSHDALCTSCTAFPLSTRVPGTEECKRAVIDFVAFQDISIKRLQRLLQALETPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              |||||||||||||:|||::|||||| |||||||||||||||||||||||||||||||| |
Db        241 GWGPTPRAGRAALRLKLQQRLTELLEAQDGALLVRLLQALRVARMPGLERSVRERFLPGH 300


RESULT 37
AAB03622
ID   AAB03622 standard; Protein; 300 AA.
XX
AC   AAB03622;
XX
DT   03-JAN-2001  (first entry)
XX
DE   Monkey Fas ligand inhibitor FLINT.
XX
KW   Monkey; Fas ligand inhibitor; FLINT; apoptosis; autoimmune disease;
KW   inflammation; infectious disease; ischaemia; Alzheimer's disease;
KW   Parkinson's disease; Crohn's disease; transplantation.
XX
OS   Primate.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..29
FT                   /label= signal_peptide
FT   Protein         30..300
FT                   /label= mature_FLINT
FT   Domain          1..42
FT                   /label= domain_1
FT   Domain          43..85
FT                   /label= domain_2
FT   Domain          86..122
FT                   /label= domain_3
FT   Domain          123..165
FT                   /label= domain_4
XX
PN   WO200034782-A1.
XX
PD   15-JUN-2000.
XX
PF   07-DEC-1999;   99WO-US28696.
XX
PR   09-DEC-1998;   98US-0111575.
PR   09-DEC-1998;   98US-0111580.
PR   07-JAN-1999;   99US-0115069.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Rosteck PRJ,  Song HY,  Su EW;
XX
DR   WPI; 2000-431379/37.
DR   N-PSDB; AAA53209.
XX
PT   Novel monkey Fas ligand inhibitor polypeptides, useful for treating
PT   inflammatory or autoimmune disease such as rheumatoid arthritis,
PT   infectious diseases such as chronic hepatitis, and
PT   Ischaemia/Re-perfusion conditions -
XX
PS   Claim 18; Page 97-99; 101pp; English.
XX
CC   The present sequence is the protein sequence of the monkey Fas ligand
CC   inhibitor (FLINT). The FLINT protein is involved in cell-specific
CC   apoptosis, and can be used to treat inflammatory and autoimmune diseases
CC   such as rheumatoid arthritis, inflammatory bowel disease,
CC   graft-versus-host disease, diabetes, psoriasis and Graves' disease,
CC   infectious diseases such as HIV-induced lymphopenia, fulminant viral
CC   hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated
CC   ulceration, ischaemia and reperfusion conditions including acute
CC   myocardial infarction, acute coronary syndrome, congestive heart failure
CC   and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute lung
CC   injury and acute respiratory distress syndrome, Crohn's disease, brain
CC   trauma and injury, chronic glomerulonephritis, osteoporosis, aplastic
CC   anaemia, myelodysplasia, ulcerative colitis, Down's syndrome, and
CC   multiple sclerosis. In addition, the protein and its gene can be used to
CC   prevent apoptosis following organ transplantation.
XX
SQ   Sequence   300 AA;

  Query Match             91.9%;  Score 1502;  DB 21;  Length 300;
  Best Local Similarity   91.3%;  Pred. No. 4e-111;
  Matches  274;  Conservative    8;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||| ||||| |||||| |||:||  | ||||||| :||| |||||||||||||:
Db          1 MRALEGPGLLLLCLVWALPALLLVPAMRGATEAPTYPWRDTDTGEWLVCAQCPPGTFVQQ 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARPCHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              |||||||||| |||| ||:|||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHALCPPGTGVMAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              |||||||||| |||||| ||||||||| |||:|||||||||||||||||||||||||| |
Db        181 LNVPGSSSHDALCTSCTAFPLSTRVPGTEECKRAVIDFVAFQDISIKRLQRLLQALETPG 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              |||||||||||||:|||::|||||| |||||||||||||||||||||||||||||||| |
Db        241 GWGPTPRAGRAALRLKLQQRLTELLEAQDGALLVRLLQALRVARMPGLERSVRERFLPGH 300


RESULT 38
AAB03624
ID   AAB03624 standard; Protein; 300 AA.
XX
AC   AAB03624;
XX
DT   03-JAN-2001  (first entry)
XX
DE   Human Fas ligand inhibitor FLINT mutant.
XX
KW   Human; Fas ligand inhibitor; FLINT; apoptosis; autoimmune disease;
KW   inflammation; infectious disease; ischaemia; Alzheimer's disease;
KW   Parkinson's disease; Crohn's disease; transplantation; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..29
FT                   /label= signal_peptide
FT   Domain          1..42
FT                   /label= domain_1
FT   Misc-difference 10
FT                   /note= "wild-type Ser substituted by Leu, Thr, Val,
FT                   Ile, Gly or Ala"
FT   Misc-difference 16
FT                   /note= "wild-type Leu substituted by Ile, Val, Ala
FT                   or Gly"
FT   Misc-difference 23
FT                   /note= "wild-type Pro substituted by Leu, Ile, Val,
FT                   Ala or Gly"
FT   Misc-difference 27
FT                   /note= "wild-type Val is substituted by Gly, Ala,
FT                   Leu or Ile"
FT   Misc-difference 30
FT                   /note= "wild-type Val substituted by Ala, Gly, Leu
FT                   or Ile"
FT   Misc-difference 31
FT                   /note= "wild-type Ala substituted by Gly, Val, Ile
FT                   or Leu"
```

```
FT   Misc-difference 33
FT                   /note= "wild-type Thr substituted by Ala, Ser, Gly,
FT                   Leu, Val or Ile"
FT   Misc-difference 41
FT                   /note= "wild-type Ala substituted by Thr, Gly, Val,
FT                   Leu or Ile"
FT   Misc-difference 42
FT                   /note= "wild-type Glu substituted by Asn or Gln"
FT   Domain          43..85
FT                   /label= domain_2
FT   Misc-difference 46
FT                   /note= "wild-type Arg substituted by His or Lys"
FT   Misc-difference 60
FT                   /note= "wild-type Arg substituted by His or Lys"
FT   Domain          86..122
FT                   /label= domain_3
FT   Misc-difference 104
FT                   /note= "wild-type Ala substituted by Gly, Val, Leu
FT                   or Ile"
FT   Domain          123..165
FT                   /label= domain_4
FT   Misc-difference 131
FT                   /note= "wild-type Ser substituted by Leu, Thr, Ile,
FT                   Ala or Gly"
FT   Misc-difference 136
FT                   /note= "wild-type Ala substituted by Gly, Val, Leu
FT                   or Ile"
FT   Misc-difference 139
FT                   /note= "wild-type Ile substituted by Leu, Gly, Ala
FT                   or Val"
FT   Misc-difference 191
FT                   /note= "wild-type Thr substituted by Ala, Ser, Gly,
FT                   Leu, Ile or Val"
FT   Misc-difference 198
FT                   /note= "wild-type Gly substituted by Ala, Val, Ile
FT                   or Leu"
FT   Misc-difference 208
FT                   /note= "wild-type Ala substituted by Gly, Leu, Val
FT                   or Ile"
FT   Misc-difference 212
FT                   /note= "wild-type Glu substituted by Asp, Asn or
FT                   Gln"
FT   Misc-difference 238
FT                   /note= "wild-type Ala substituted by Gly, Leu, Val
FT                   or Ile"
FT   Misc-difference 254
FT                   /note= "wild-type Gln substituted by Arg, Asn, Asp,
FT                   Glu, Lys or His"
FT   Misc-difference 258
FT                   /note= "wild-type Arg substituted by Gln, Lys, His,
FT                   Asn, Asp or Glu"
FT   Misc-difference 259
FT                   /note= "wild-type Arg substituted by Gln, Lys, His,
FT                   Asn, Asp or Glu"
FT   Misc-difference 266
FT                   /note= "wild-type Gly substituted by Glu, Asn, Gln,
FT                   Ala, Val, Leu, Ile or Asp"
FT   Misc-difference 299
FT                   /note= "wild-type Val substituted by Gly, Leu, Ile
FT                   or Ala"
XX
PN   WO200034782-A1.
XX
PD   15-JUN-2000.
XX
PF   07-DEC-1999;   99WO-US28696.
XX
PR   09-DEC-1998;   98US-0111575.
PR   09-DEC-1998;   98US-0111580.
PR   07-JAN-1999;   99US-0115069.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Rosteck PRJ,  Song HY,  Su EW;
XX
DR   WPI; 2000-431379/37.
XX
PT   Novel monkey Fas ligand inhibitor polypeptides, useful for treating
PT   inflammatory or autoimmune disease such as rheumatoid arthritis,
PT   infectious diseases such as chronic hepatitis, and
PT   Ischaemia/Re-perfusion conditions -
XX
PS   Claim 3; Page -; 101pp; English.
XX
CC   The present sequence is a mutant protein sequence of the human Fas
CC   ligand inhibitor (FLINT). The FLINT protein is involved in cell-specific
CC   apoptosis, and can be used to treat inflammatory and autoimmune diseases
CC   such as rheumatoid arthritis, inflammatory bowel disease,
CC   graft-versus-host disease, diabetes, psoriasis and Graves' disease,
CC   infectious diseases such as HIV-induced lymphopenia, fulminant viral
CC   hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated
CC   ulceration, ischaemia and reperfusion conditions including acute
CC   myocardial infarction, acute coronary syndrome, congestive heart failure
CC   and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute
CC   lung injury and acute respiratory distress syndrome, Crohn's disease,
CC   brain trauma and injury, chronic glomerulonephritis, osteoporosis,
CC   aplastic anaemia, myelodysplasia, ulcerative colitis, Down's syndrome,
CC   and multiple sclerosis. In addition, the protein and its gene can be used
CC   to prevent apoptosis following organ transplantation.
CC   Note: The present sequence is not shown in the specification but is
CC   derived from the Homo sapiens wild-type FLINT sequence shown on page
CC   91-93 (AAB03621).
XX
SQ   Sequence   300 AA;

  Query Match             91.9%;  Score 1502;  DB 21;  Length 300;
  Best Local Similarity   91.7%;  Pred. No. 4e-111;
  Matches  275;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||| ||||| |||||| ||| || | | ||||||| ||| ||||||||||||
Db          1 MRALEGPGLXLLCLVXALPALLXVPAXRGXXEXPTYPWRDXXTGEXLVCAQCPPGTFVQX 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARXCHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              |||||||||| |||| || |||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHAXCPPGXGVXAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              |||||||||| |||||| ||||||||| ||| ||||||||||||||||||||||||||| ||
Db        181 LNVPGSSSHDXLCTSCTXFPLSTRVPGXEECXRAVIDFVAFQDISIKRLQRLLQALEXPE 240

Qy        241 GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              |||||||||||||| |||  |||||| |||||||||||||||||||||||||||||||| |
Db        241 GWGPTPRAGRAALXLKLXXRLTELLXAQDGALLVRLLQALRVARMPGLERSVRERFLPXH 300


RESULT 39
AAY42184
ID   AAY42184 standard; Protein; 271 AA.
XX
AC   AAY42184;
XX
DT   17-DEC-1999  (first entry)
XX
DE   Human mFLINT #1 protein sequence.
XX
KW   Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
KW   apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW   sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW   reperfusion-associated injury; aplastic anaemia; differentiation;
KW   growth; myelodysplastic syndrome; pancytopenic condition;
KW   myocardial ischaemia.
```

```
XX
OS   Homo sapiens.
XX
PN   WO9950413-A2.
XX
PD   07-OCT-1999.
XX
PF   30-MAR-1999;   99WO-US06797.
XX
PR   30-MAR-1998;   98US-0079856.
PR   20-MAY-1998;   98US-0086074.
PR   09-SEP-1998;   98US-0099643.
PR   17-DEC-1998;   98US-0112577.
PR   18-DEC-1998;   98US-0112703.
PR   18-DEC-1998;   98US-0112933.
PR   22-DEC-1998;   98US-0113407.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Bumol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;
PI   Hui KY, Kharitonenkov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;
PI   Song HY, Wang J, Wu X, Zuckerman SH;
XX
DR   WPI; 1999-591319/50.
DR   N-PSDB; AAZ25377.
XX
PT   Use of mature FLINT for treating acute liver failure, inflammation,
PT   cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic
PT   and proinflammatory activity
XX
PS   Claim 31; Fig 3; 99pp; English.
XX
CC   The present invention describes therapeutic applications of mature FLINT
CC   (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
CC   (mFLINT), which is a member of the tumour necrosis factor receptor
CC   superfamily, is used for treating acute liver failure, inflammation of
CC   the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
CC   with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
CC   injury or disorder such as hypercoagulation (including use with
CC   thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
CC   or disorder, Type I diabetes, cancer, cell damage or damage to an
CC   innocent bystander tissue that is induced by a chemotherapeutic agent or
CC   therapeutic irradiation, treating haematopoietic progenitor cells that
CC   have been exposed to therapeutic radiation or chemotherapy, aplastic
CC   anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
CC   also used for promoting the growth or differentiation of a haematopoietic
CC   progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
CC   resulting from abnormal myocardial ischaemia. The present sequence
CC   represents human mFLINT.
XX
SQ   Sequence   271 AA;

  Query Match             91.2%;  Score 1491;  DB 20;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-110;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 40
AAB19334
ID   AAB19334 standard; Protein; 271 AA.
XX
AC   AAB19334;
XX
DT   19-FEB-2001  (first entry)
XX
DE   A mature human FAS Ligand Inhibitory Protein (FLINT).
XX
KW   Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;
KW   tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;
KW   acute respiratory distress syndrome; ulcerative colitis;
KW   chronic obstructive pulmonary disease; Crohn's disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "optionally replaced with Met"
FT   Misc-difference 2
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 4
FT                   /note= "optionally replaced with Ala"
FT   Misc-difference 12
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 13
FT                   /note= "optionally replaced with Asp or Gln"
FT   Misc-difference 17
FT                   /note= "optionally replaced with Trp"
FT   Misc-difference 25
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 34
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 35
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 36
FT                   /note= "optionally replaced with Thr"
FT   Misc-difference 37
FT                   /note= "optionally replaced with Asn or Thr"
FT   Misc-difference 38
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 53
FT                   /note= "optionally replaced with Asp"
FT   Misc-difference 63
FT                   /note= "optionally replaced with Trp"
FT   Misc-difference 67
FT                   /note= "optionally replaced with Asp"
FT   Misc-difference 69
FT                   /note= "optionally replaced with Glu"
FT   Misc-difference 75
FT                   /note= "optionally replaced with Pro"
FT   Misc-difference 82
FT                   /note= "optionally replaced with Glu or Thr"
FT   Misc-difference 88
FT                   /note= "optionally replaced with Pro"
FT   Misc-difference 94
FT                   /note= "optionally replaced with Tyr"
FT   Misc-difference 95
FT                   /note= "optionally replaced with Asp"
FT   Misc-difference 96
FT                   /note= "optionally replaced with Gln"
FT   Misc-difference 101
FT                   /note= "optionally replaced with Thr"
FT   Misc-difference 102
FT                   /note= "optionally replaced with Leu"
FT   Misc-difference 104
FT                   /note= "optionally replaced with Ser"
FT   Misc-difference 107
```

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FT                   /note= "optionally replaced with Ser, Asp, Glu or Thr"
FT   Misc-difference 110
FT                   /note= "optionally replaced with Met, Thr or Glu"
FT   Misc-difference 114
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 115
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 126
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 132
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 134
FT                   /note= "optionally replaced with Thr"
FT   Misc-difference 162
FT                   /note= "optionally replaced with Ala"
FT   Misc-difference 166
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 169
FT                   /note= "optionally replaced with Ala"
FT   Misc-difference 171
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 172
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 179
FT                   /note= "optionally replaced with Thr"
FT   Misc-difference 183
FT                   /note= "optionally replaced with Lys"
FT   Misc-difference 194
FT                   /note= "optionally replaced with Asn"
FT   Misc-difference 196
FT                   /note= "optionally replaced with Thr"
FT   Misc-difference 209
FT                   /note= "optionally replaced with Thr"
FT   Misc-difference 225
FT                   /note= "optionally replaced with Arg"
FT   Misc-difference 237
FT                   /note= "optionally replaced with Glu"
FT   Misc-difference 270
FT                   /note= "optionally replaced with Gly"
XX
PN   WO200058465-A2.
XX
PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-US06417.
XX
PR   30-MAR-1999;   99US-0126839.
PR   21-JUN-1999;   99US-0140077.
PR   21-JUN-1999;   99US-0140156.
PR   20-OCT-1999;   99US-0160566.
PR   18-FEB-2000; 2000US-0183398.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JE, Micanovic R;
PI   Newton CM, Noblitt TW, Rathmachalam R, Tschang SR, Witcher DR;
PI   Wroblewski VJ;
XX
DR   WPI; 2000-656167/63.
DR   N-PSDB; AAA75999.
XX
PT   FAS Ligand Inhibitory Protein analogs useful for treating abnormal
PT   apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,
PT   chronic obstructive pulmonary disease ulcerative colitis or Crohn's
PT   disease -
XX
PS   Claim 1; Page 112-113; 114pp; English.
XX
CC   The present sequence represents a mature human FAS Ligand Inhibitory
CC   Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor
CC   proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature
CC   FLINT protein is modified to produce analogues, which have greater
CC   potency, longer in vivo half-lives, decreased aggregation, decreased
CC   absorption onto surfaces, increased solubility and improved ease of
CC   formulation. The FLINT analogue is useful for treating a patient
CC   suffering from disease or condition relating to abnormal apoptosis such
CC   as acute lung injury, acute respiratory distress syndrome, pulmonary
CC   fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
CC   Crohn's disease.
XX
SQ   Sequence   271 AA;

  Query Match             91.2%;  Score 1491;  DB 21;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-110;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy          90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy         150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy         210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy         270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
               ||||||||||||||||||||||||||||||
Db         241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 41
AAB19705
ID   AAB19705 standard; Protein; 271 AA.
XX
AC   AAB19705;
XX
DT   05-FEB-2001  (first entry)
XX
DE   Human FAS ligand inhibitor protein FLINT.
XX
KW   FLINT; FAS ligand inhibitory protein; human; protease resistant;
KW   acute lung injury; acute respiratory distress syndrome;
KW   chronic obstructive pulmonary disease; pulmonary fibrosis;
KW   ulcerative colitis; therapy; organ transplantation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Cleavage-site   218..219
FT                   /note= "cleaved by trypsin-like proteases"
FT   Misc-difference 34
FT                   /note= "optionally replaced by Arg, as given in
FT                   Claims 10, 11, 13 and 14"
FT   Misc-difference 36
FT                   /note= "optionally replaced by Thr, as given in
FT                   Claims 10, 11, 13 and 14"
FT   Misc-difference 132
FT                   /note= "optionally replaced by Asn, as given in
FT                   Claim 12"
FT   Misc-difference 194
FT                   /note= "optionally replaced by Asn, as given in
FT                   Claims 11 and 14"
FT   Misc-difference 196
FT                   /note= "optionally replaced by Thr, as given in
FT                   Claims 11 and 14"
FT   Misc-difference 214
FT                   /note= "optionally replaced by any naturally
FT                   occurring amino acid"
FT   Misc-difference 215
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FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid"
FT   Misc-difference 216
FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid, preferably Pro as
FT                          given in Claims 9 and 15"
FT   Misc-difference 217
FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid, preferably Tyr as
FT                          given in Claim 9"
FT   Misc-difference 218
FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid, preferably Gln, Glu,
FT                          Ala, Gly, Ser, Val, Tyr or Asn as given in
FT                          Claims, 9, 10, 11, 12, especially Gln as
FT                          given in Claims 13, 14, 15, 35 and 36"
FT   Misc-difference 219
FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid"
FT   Misc-difference 220
FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid"
FT   Misc-difference 221
FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid"
FT   Misc-difference 222
FT                   /note= "optionally replaced by any naturally
FT                          occurring amino acid"
XX
PN   WO200058466-A2.
XX
PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-US06418.
XX
PR   30-MAR-1999;   99US-0126839.
PR   21-JUN-1999;   99US-0140073.
PR   04-AUG-1999;   99US-0147071.
PR   20-OCT-1999;   99US-0160524.
PR   21-OCT-1999;   99US-0160669.
PR   20-DEC-1999;   99US-0172744.
PR   26-JAN-2000; 2000US-0178184.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Rathnachalam R,  Witcher DR;
XX
DR   WPI; 2000-664925/64.
DR   N-PSDB; AAA88730.
XX
PT   Novel protease resistant FAS ligand inhibitory protein analogues
PT   resistant to in vivo or in vitro proteolysis at amino acid position 218
PT   of the mature protein, useful for treating autoimmune diseases
XX
PS   Claim 1; Page 94-95; 100pp; English.
XX
CC   The present sequence is that of human FAS ligand inhibitory protein
CC   FLINT mature protein.  FLINT is a tumour necrosis factor receptor
CC   homologue that binds FAS ligand, preventing its interaction with
CC   FAS.  This interaction is implicated in runaway apoptosis and
CC   inflammatory disease.  FLINT also binds to LIGHT, a membrane-bound
CC   ligand, which may play a role in immune modulation and apoptosis.
CC   The invention relates to novel FLINT analogues (see also AAB19706-09)
CC   that are resistant to proteolysis by trypsin-like proteases between
CC   positions 218 and 219 of the FLINT mature protein sequence.  The
CC   analogues have amino acid substitutions in the region comprising
CC   amino acids 214-222, and may contain additional substitutions at
CC   residues 34, 36, 132, 194 and/or 196.  Nucleic acids, vectors and
CC   transformed host cells for recombinant production of the analogues
CC   are claimed.  FLINT cDNA (see AAA88730) is used as a template for
CC   introducing the required point mutations.  The protease resistant
CC   FLINT analogues are used to prevent or treat acute lung injury,
CC   acute respiratory stress syndrome, ulcerative colitis, chronic
CC   obstructive pulmonary disease, pulmonary fibrosis, to inhibit T
CC   lymphocyte activation, and to facilitate organ preservation for
CC   transplantation (claimed).
XX
SQ   Sequence   271 AA;

  Query Match             91.2%;  Score 1491;  DB 21;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-110;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 42
AAY97247
ID   AAY97247 standard; Protein; 271 AA.
XX
AC   AAY97247;
XX
DT   19-DEC-2000  (first entry)
XX
DE   M68 TNF receptor related protein (mature protein).
XX
KW   M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;
KW   receptor; immune response; cell differentiation; ligand; cancer;
KW   bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
KW   Grave's disease; idiopathic myxodema; autoimmune diabetes;
KW   thrombotic thrombocytopenic purpura; multiple sclerosis;
KW   liver diseases; autoimmune gastritis; ulcerative colitis;
KW   glomerulonephritis; pulmonary fibrosis; heart failure;
KW   atherosclerosis; aplastic anaemia; myelodisplastic syndromes;
KW   osteoporosis; Alzheimers disease; Parkinsons disease; stroke;
KW   myocardial infarction; human.
XX
OS   Homo sapiens.
XX
PN   WO200046247-A1.
XX
PD   10-AUG-2000.
XX
PF   04-FEB-2000; 2000WO-US03037.
XX
PR   05-FEB-1999;   99US-0118902.
PR   20-DEC-1999;   99US-0172754.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Bai C;
XX
DR   WPI; 2000-506066/45.
XX
PT   Isolated human M68 nucleic acids and proteins which are part of the
PT   tumor necrosis factor receptor (TNFR) family, useful for identifying
PT   modulators that may be used to treat various diseases e.g. cancer,
PT   osteoporosis, Alzheimer's disease
```

```
XX
PS   Claim 1; Page 76; 80pp; English.
XX
CC   The M68 protein is a member of a family of proteins which have
CC   roles in immune responses, cell death, cell proliferation and
CC   stimulation of cell differentiation. M68 lacks a transmembrane domain
CC   and is a secreted factor suggesting that it functions as a natural
CC   inhibitor for its ligand. The altered expression pattern of M68 in a
CC   multitude of tissues suggests that M68 may play a role in cancer by
CC   binding to its ligand and blocking apoptotic cell death induced by
CC   such a ligand. This anti-apoptopic role of M68 suggests that
CC   modulators of M68 will be useful in treatment of apoptosis-related
CC   diseases such as various forms of cancer and various bone disorders.
CC   M68 nucleic acids and proteins are therefore useful for treating
CC   conditions involving atypical apoptosis and for identifying
CC   modulators of M68. Modulators of M68 are useful for treatment of
CC   cancer and other diseases associated with abnormal levels of
CC   apoptosis including systemic lupus erythematosus, Hashimoto's
CC   thyroiditis, Grave's disease, idiopathic myxodema, autoimmune
CC   diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,
CC   liver diseases, autoimmune gastritis, ulcerative colitis,
CC   glomerulonephritis, pulmonary fibrosis, heart failure,
CC   atherosclerosis, aplastic anaemia, myelodisplastic syndromes,
CC   osteoporosis, Alzheimers disease, Parkinsons disease, stroke, and
CC   myocardial infarction.
XX
SQ   Sequence   271 AA;

  Query Match             91.2%;  Score 1491;  DB 21;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-110;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 43
AAY96598
ID   AAY96598 standard; Protein; 271 AA.
XX
AC   AAY96598;
XX
DT   26-SEP-2000  (first entry)
XX
DE   Human mature FLINT.
XX
KW   FLINT; osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNFR;
KW   FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
KW   anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
KW   anti-inflammatory; antibacterial; immunosuppressive.
XX
OS   Homo sapiens.
XX
PN   WO200037094-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;   99WO-US30734.
XX
PR   22-DEC-1998;   98US-0113407.
PR   30-MAR-1999;   99WO-US06797.
PR   20-OCT-1999;   99US-0172239.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Cohen FJ,  Posada JA,  Wierda D;
XX
DR   WPI; 2000-475441/41.
DR   N-PSDB; AAA51077.
XX
PT   Use of mature FLINT for treating e.g. acute respiratory distress
PT   syndrome, ulcerative colitis or ischemic injury during organ
PT   transplantation
XX
PS   Example 8; Fig 3; 125pp; English.
XX
CC   Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis
CC   factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
CC   prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
CC   mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
CC   treating acute respiratory distress syndrome, treating or inhibiting
CC   ulcerative colitis, inhibiting ischemic injury during organ
CC   transplantation or for organ preservation during transplantation. mFLINT
CC   can also be used to treat acute liver failure, inflammation of the liver,
CC   abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
CC   inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
CC   damage to a cardiac myocyte resulting from abnormal myocardial ischaemia,
CC   Type I diabetes, cancer, damage to an innocent bystander tissue induced
CC   by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
CC   myelodysplastic syndromes and pancytopenic conditions.
XX
SQ   Sequence   271 AA;

  Query Match             91.2%;  Score 1491;  DB 21;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-110;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 44
AAE03567
ID   AAE03567 standard; Protein; 271 AA.
XX
AC   AAE03567;
XX
DT   04-AUG-2001  (first entry)
XX
DE   Human mature fas ligand inhibitory protein (FLINT).
XX
KW   Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
```

```
KW   TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;
KW   acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;
KW   chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;
KW   rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis;
KW   fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;
KW   chronic renal failure; graft-vs-host disease; cutaneous inflammation;
KW   vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;
KW   insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;
KW   Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;
KW   Down's syndrome; multiple sclerosis; cytostatic; nootropic;
KW   neuroprotective; vasotropic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   144
FT                   /note= "N-linked glycosylation site"
FT   Modified-site   174
FT                   /note= "O-linked glycosylation site"
FT   Modified-site   216
FT                   /note= "O-linked glycosylation site"
FT   Cleavage-site   218..219
FT                   /note= "Proteolytic cleavage"
XX
PN   WO200142463-A1.
XX
PD   14-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-US30166.
XX
PR   07-DEC-1999;   99US-0169367.
PR   07-DEC-1999;   99US-0169381.
PR   07-DEC-1999;   99US-0169412.
PR   23-MAR-2000; 2000US-0191430.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Lu J,  Witcher DR;
XX
DR   WPI; 2001-381684/40.
DR   N-PSDB; AAD07380.
XX
PT   New FLINT polypeptide for treating and/or preventing acute lung injury,
PT   acute respiratory distress syndrome, ulcerative colitis, and
PT   graft-versus-host disease, comprises O-linked or N-linked
PT   oligosaccharides -
XX
PS   Example 1; Page 52-53; 60pp; English.
XX
CC   The present sequence is human mature fas ligand inhibitory protein
CC   (FLINT). FLINT, a homologue of tumour necrosis factor receptor
CC   protein (TNFR), binds fas ligand (FasL) and thereby preventing the
CC   interaction of FasL with fas. FLINT comprising O-linked or N-linked
CC   oligosaccharides is useful for preventing or treating acute lung injury
CC   (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,
CC   chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),
CC   to facilitate organ preservation for transplantation and to inhibit T
CC   lymphocyte activation. FLINT is useful for treating and/or preventing
CC   diseases such as rheumatoid arthritis, fibroproliferative lung disease,
CC   fibrotic lung disease, acute lung injury, human immunodeficiency virus
CC   (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-
CC   host disease, cutaneous inflammation, vascular leak syndrome,
CC   Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent
CC   diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,
CC   Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as
CC   psoriasis, Down's syndrome, and multiple sclerosis.
XX
SQ   Sequence   271 AA;

  Query Match             91.2%;  Score 1491;  DB 22;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-110;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy          90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy         150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy         210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy         270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
               ||||||||||||||||||||||||||||||
Db         241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 45
AAB68044
ID   AAB68044 standard; Protein; 271 AA.
XX
AC   AAB68044;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Amino acid sequence of a human mature FLINT polypeptide.
XX
KW   FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;
KW   Fas ligand; acute liver failure; cerebral ischemia; apoptosis.
XX
OS   Homo sapiens.
XX
PN   WO200118055-A1.
XX
PD   15-MAR-2001.
XX
PF   31-AUG-2000; 2000WO-US20807.
XX
PR   10-SEP-1999;   99US-0153339.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Atkinson PR,  Tian Y,  Witcher DR;
XX
DR   WPI; 2001-273382/28.
XX
PT   Compositions comprising a divalent metal cation and a FAS Ligand
PT   Inhibitory Protein (FLINT), for reducing or inducing aggregation of
PT   FLINT and for treating diseases involving FasL/Fas and/or
PT   LIGHT/LT-beta-R receptor interactions   -
XX
PS   Example 1; Page 39-40; 44pp; English.
XX
CC   The present sequence represents a mature FLINT (FAS Ligand Inhibitory
CC   Protein) polypeptide. The specification describers a composition
CC   comprising a divalent metal cation and FLINT protein. The composition
CC   is used either for reducing, reversing or eliminating aggregation and
CC   precipitation of FLINT or for inducing oligomerisation or aggregation
CC   of FLINT molecules. They can be used for purifying FLINT and/or
CC   maintaining FLINT in solution. The compositions are used to treat
CC   and/or prevent disorders associated with the binding of Fas to FasL
CC   and/or LIGHT to the LTbetaR and/or TR2/HVEM receptors. Uses include the
CC   treatment of acute liver failure and cerebral ischemia and the prevention
CC   of apoptosis.
XX
SQ   Sequence   271 AA;

  Query Match             91.2%;  Score 1491;  DB 22;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-110;
```

```
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 46
AAB68047
ID   AAB68047 standard; Protein; 271 AA.
XX
AC   AAB68047;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Amino acid sequence of a human mature FLINT polypeptide.
XX
KW   FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;
KW   Fas ligand; acute liver failure; cerebral ischemia; apoptosis.
XX
OS   Homo sapiens.
XX
PN   WO200118041-A2.
XX
PD   15-MAR-2001.
XX
PF   31-AUG-2000; 2000WO-US20805.
XX
PR   10-SEP-1999;   99US-0153445.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Atkinson PR,  Tian Y,  Witcher DR;
XX
DR   WPI; 2001-273381/28.
XX
PT   Compositions comprising a divalent metal cation and a FAS Ligand
PT   Inhibitory Protein (FLINT), for reducing or inducing aggregation of
PT   FLINT and for treating diseases involving FasL/Fas and/or
PT   LIGHT/LT-beta-R receptor interactions  -
XX
PS   Disclosure; Page 30-31; 33pp; English.
XX
CC   The present sequence represents a human mature FLINT (FAS Ligand
CC   Inhibitory Protein) polypeptide. The specification describers a
CC   composition comprising a divalent metal cation and FLINT protein. The
CC   composition is used either for reducing, reversing or eliminating
CC   aggregation and precipitation of FLINT or for inducing oligomerisation
CC   or aggregation of FLINT molecules. They can be used for purifying FLINT
CC   and/or maintaining FLINT in solution. The compositions are used to treat
CC   and/or prevent disorders associated with the binding of Fas to FasL
CC   and/or LIGHT to the LTbetaR and/or TR2/HVEM receptors. Uses include the
CC   treatment of acute liver failure and cerebral ischemia and the prevention
CC   of apoptosis.
XX
SQ   Sequence   271 AA;

  Query Match           91.2%;  Score 1491;  DB 22;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-110;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 47
AAB74465
ID   AAB74465 standard; protein; 271 AA.
XX
AC   AAB74465;
XX
DT   30-MAY-2001  (first entry)
XX
DE   Human FLINT mature protein.
XX
KW   Human; FLINT; FAS ligand inhibitory protein; analogue; apoptosis;
KW   inflammatory disease.
XX
OS   Homo sapiens.
XX
PN   WO200118202-A2.
XX
PD   15-MAR-2001.
XX
PF   31-AUG-2000; 2000WO-US20806.
XX
PR   10-SEP-1999;   99US-0153433.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Atkinson PR,  Tian Y,  Witcher DR;
XX
DR   WPI; 2001-257796/26.
XX
PT   Compositions useful for reducing/inducing aggregation of a FLINT analog
PT   comprise a divalent metal cation and a protease-resistant FAS Ligand
PT   Inhibitory Protein (FLINT) analog -
XX
PS   Claim 4; Page 41-42; 44pp; English.
XX
CC   The present invention describes a composition comprising a divalent metal
CC   cation associated with a protease resistant Fas ligand inhibitory protein
CC   (FLINT) analogue. The composition is useful in the treatment of diseases
CC   associated with Fas binding to its ligand, such as acute liver failure,
CC   inflammatory diseases, cerebral ischaemia and apoptosis. The present
CC   sequence is the mature FLINT protein.
XX
SQ   Sequence   271 AA;

  Query Match           91.2%;  Score 1491;  DB 22;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-110;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
```

RESULT 48
AAE14578
ID AAE14578 standard; Protein; 271 AA.
XX
AC AAE14578;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human mature FLINT protein.
XX
KW FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW organ failure; liver; kidney; pancreas; inflammatory disease;
KW neutrophil; sepsis; acute respiratory distress syndrome;
KW acute lung injury; systemic inflammatory response syndrome; SIRS;
KW multiple organ dysfunction; MODS; human.
XX
OS Homo sapiens.
XX
PN WO200209668-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-US21105.
XX
PR 02-AUG-2000; 2000US-222476P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Micanovic R, Witcher DR;
XX
DR WPI; 2002-206149/26.
DR N-PSDB; AAD27868.
XX
PT Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT useful for treating e.g. sepsis or respiratory distress syndrome,
PT involves pulmonary administration of a therapeutic amount of the FLINT
PT or FLINT analog -
XX
PS Disclosure; Page 29-30; 35pp; English.
XX
CC The invention relates to a new method of administering FLINT
CC (FAS ligand inhibitory protein) or FLINT analog that involves pulmonary
CC administration of a therapeutic amount of the FLINT or FLINT analog.
CC The method enables systemic absorption of FLINT through lungs and
CC significantly reduces or eliminates the need for administering FLINT by
CC injection or other routes of administration. The method is useful in
CC treating disorders related to enhanced apoptosis (e.g. organ failure
CC in liver, kidneys and pancreas) and inflammatory diseases associated with
CC neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC multiple organ dysfunction (MODS)). The method minimises the pain
CC and discomfort of injection methods. The present sequence is human
CC mature FLINT protein.
XX
SQ Sequence 271 AA;

```
  Query Match             91.2%;  Score 1491;  DB 23;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-110;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271
```

RESULT 49
AAB19709
ID AAB19709 standard; Protein; 271 AA.
XX
AC AAB19709;
XX
DT 05-FEB-2001 (first entry)
XX
DE Protease-resistant FLINT analogue, R218Q substitution.
XX
KW FLINT; FAS ligand inhibitory protein; human; protease resistant;
KW acute lung injury; acute respiratory distress syndrome;
KW chronic obstructive pulmonary disease; pulmonary fibrosis;
KW ulcerative colitis; therapy; organ transplantation; substitution;
KW mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 218
FT /note= "Wild-type Arg substituted by Gln"
XX
PN WO200058466-A2.
XX
PD 05-OCT-2000.
XX
PF 20-MAR-2000; 2000WO-US06418.
XX
PR 30-MAR-1999; 99US-0126839.
PR 21-JUN-1999; 99US-0140073.
PR 04-AUG-1999; 99US-0147071.
PR 20-OCT-1999; 99US-0160524.
PR 21-OCT-1999; 99US-0160669.
PR 20-DEC-1999; 99US-0172744.
PR 26-JAN-2000; 2000US-0178184.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Micanovic R, Rathnachalam R, Witcher DR;
XX
DR WPI; 2000-664925/64.
XX
PT Novel protease resistant FAS ligand inhibitory protein analogues

```
PT   resistant to in vivo or in vitro proteolysis at amino acid position 218
PT   of the mature protein, useful for treating autoimmune diseases -
XX
PS   Claim 36; Page -; 100pp; English.
XX
CC   Novel human FLINT analogues are resistant to proteolysis at
CC   position 218 of the wild-type protein (see AAB19705). The present
CC   sequence is a specific example of a protease-resistant FLINT
CC   analogue in which the the Arg residue at position 218 has been
CC   substituted by a Gln residue. The FLINT analogue can be obtained
CC   by mutagenesis of template FLINT cDNA (see AAA88730) and expressed
CC   in recombinant host cells. It is used to prevent or treat acute
CC   lung injury, acute respiratory stress syndrome, ulcerative colitis,
CC   chronic obstructive pulmonary disease, and pulmonary fibrosis. It
CC   is also used to inhibit T lymphocyte activation, to inhibit
CC   ischaemic injury during organ transplantation, and as a component
CC   of a liquid medium for infusion and preservation of organs (claimed).
CC   Resistance to proteolytic cleavage greatly increases in vivo
CC   half-life.
CC   Note: The present sequence is not shown in the specification but is
CC   derived from the human FLINT mature protein sequence given in
CC   the Sequence Listing (see AAB19705).
XX
SQ   Sequence   271 AA;

  Query Match             91.0%;  Score 1487;  DB 21;  Length 271;
  Best Local Similarity   99.6%;  Pred. No. 5.5e-110;
  Matches  270;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPQAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 50
AAE03571
ID   AAE03571 standard; Protein; 271 AA.
XX
AC   AAE03571;
XX
DT   04-AUG-2001  (first entry)
XX
DE   Human mature fas ligand inhibitory protein (FLINT) variant, R218Q.
XX
KW   Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
KW   TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;
KW   acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;
KW   chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;
KW   rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis;
KW   fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;
KW   chronic renal failure; graft-vs-host disease; cutaneous inflammation;
KW   vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;
KW   insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;
KW   Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;
KW   Down's syndrome; multiple sclerosis; cytostatic; nootropic;
KW   neuroprotective; vasotropic; mutant; mutein; variant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 218
FT                   /note= "Wild type Arg substituted with Gln"
XX
PN   WO200142463-A1.
XX
PD   14-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-US30166.
XX
PR   07-DEC-1999;   99US-0169367.
PR   07-DEC-1999;   99US-0169381.
PR   07-DEC-1999;   99US-0169412.
PR   23-MAR-2000; 2000US-0191430.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Lu J,  Witcher DR;
XX
DR   WPI; 2001-381684/40.
XX
PT   New FLINT polypeptide for treating and/or preventing acute lung injury,
PT   acute respiratory distress syndrome, ulcerative colitis, and
PT   graft-versus-host disease, comprises O-linked or N-linked
PT   oligosaccharides -
XX
PS   Example 1; Page -; 60pp; English.
XX
CC   The present sequence is human mature fas ligand inhibitory protein
CC   (FLINT) variant, R218Q. FLINT, a homologue of tumour necrosis factor
CC   receptor protein (TNFR), binds fas ligand (FasL) and thereby preventing
CC   the interaction of FasL with fas. FLINT comprising O-linked or N-linked
CC   oligosaccharides is useful for preventing or treating acute lung injury
CC   (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,
CC   chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),
CC   to facilitate organ preservation for transplantation and to inhibit T
CC   lymphocyte activation. FLINT is useful for treating and/or preventing
CC   diseases such as rheumatoid arthritis, fibroproliferative lung disease,
CC   fibrotic lung disease, acute lung injury, human immunodeficiency virus
CC   (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-
CC   host disease, cutaneous inflammation, vascular leak syndrome,
CC   Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent
CC   diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,
CC   Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as
CC   psoriasis, Down's syndrome, and multiple sclerosis.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the mature FLINT sequence shown as SEQ ID NO:1 (AAE03567)
CC   in sequence listing of the specification.
XX
SQ   Sequence   271 AA;

  Query Match             91.0%;  Score 1487;  DB 22;  Length 271;
  Best Local Similarity   99.6%;  Pred. No. 5.5e-110;
  Matches  270;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPQAGRAALQLKLRRRLTELLGAQD 240
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```
Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 51
AAB74467
ID   AAB74467 standard; protein; 271 AA.
XX
AC   AAB74467;
XX
DT   30-MAY-2001  (first entry)
XX
DE   Human FLINT mature protein mutant R218Q.
XX
KW   Human; FLINT; FAS ligand inhibitory protein; analogue; apoptosis;
KW   inflammatory disease; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 218
FT                   /note= "wild-type Arg substituted by Gln"
XX
PN   WO200118202-A2.
XX
PD   15-MAR-2001.
XX
PF   31-AUG-2000; 2000WO-US20806.
XX
PR   10-SEP-1999;   99US-0153433.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Atkinson PR,  Tian Y,  Witcher DR;
XX
DR   WPI; 2001-257796/26.
XX
PT   Compositions useful for reducing/inducing aggregation of a FLINT analog
PT   comprise a divalent metal cation and a protease-resistant FAS Ligand
PT   Inhibitory Protein (FLINT) analog -
XX
PS   Claim 5; Page -; 44pp; English.
XX
CC   The present invention describes a composition comprising a divalent metal
CC   cation associated with a protease resistant Fas ligand inhibitory protein
CC   (FLINT) analogue. The composition is useful in the treatment of diseases
CC   associated with Fas binding to its ligand, such as acute liver failure,
CC   inflammatory diseases, cerebral ischaemia and apoptosis. The present
CC   sequence is the protease resistant FLINT protein.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the wild-type FLINT protein shown in SEQ ID NO: 1 (see
CC   AAB74465).
XX
SQ   Sequence   271 AA;

  Query Match             91.0%;  Score 1487;  DB 22;  Length 271;
  Best Local Similarity   99.6%;  Pred. No. 5.5e-110;
  Matches  270;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPQAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 52
AAE14581
ID   AAE14581 standard; Protein; 271 AA.
XX
AC   AAE14581;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human protease-resistant mature FLINT analogue (R218Q).
XX
KW   FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW   organ failure; liver; kidney; pancreas; inflammatory disease;
KW   neutrophil; sepsis; acute respiratory distress syndrome;
KW   acute lung injury; systemic inflammatory response syndrome; SIRS;
KW   multiple organ dysfunction; MODS; human; protease-resistant;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 218
FT                   /note= "Wild-type Arg is replaced with Gln"
XX
PN   WO200209668-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-US21105.
XX
PR   02-AUG-2000; 2000US-222476P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Witcher DR;
XX
DR   WPI; 2002-206149/26.
XX
PT   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT   useful for treating e.g. sepsis or respiratory distress syndrome,
PT   involves pulmonary administration of a therapeutic amount of the FLINT
PT   or FLINT analog -
XX
PS   Claim 14; Page -; 35pp; English.
XX
CC   The invention relates to a new method of administering FLINT
CC   (FAS ligand inhibitory protein) or FLINT analogue that involves pulmonary
CC   administration of a therapeutic amount of the FLINT or FLINT analogue.
CC   The method enables systemic absorption of FLINT through lungs and
CC   significantly reduces or eliminates the need for administering FLINT by
CC   injection or other routes of administration. The method is useful in
CC   treating disorders related to enhanced apoptosis (e.g. organ failure
CC   in liver, kidneys and pancreas) and inflammatory diseases associated with
CC   neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC   acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC   multiple organ dysfunction (MODS)). The method minimises the pain
CC   and discomfort of injection methods. The present sequence is human
CC   protease-resistant mature FLINT analogue (R218Q).
CC   Note: The present sequence is not shown in the specification, but
CC   is derived from the mature FLINT protein sequence (SEQ ID NO:1) shown in
CC   Sequence Listing (AAE14578).
XX
SQ   Sequence   271 AA;
```

```
  Query Match             91.0%;  Score 1487;  DB 23;  Length 271;
  Best Local Similarity   99.6%;  Pred. No. 5.5e-110;
  Matches  270;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPQAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 53
AAE03584
ID   AAE03584 standard; Protein; 271 AA.
XX
AC   AAE03584;
XX
DT   04-AUG-2001  (first entry)
XX
DE   Human mature fas ligand inhibitory protein (FLINT) variant, R218E.
XX
KW   Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
KW   TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;
KW   acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;
KW   chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;
KW   rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis;
KW   fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;
KW   chronic renal failure; graft-vs-host disease; cutaneous inflammation;
KW   vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;
KW   insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;
KW   Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;
KW   Down's syndrome; multiple sclerosis; cytostatic; nootropic;
KW   neuroprotective; vasotropic; mutant; mutein; variant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 218
FT                   /note= "Wild type Arg substituted with Glu"
XX
PN   WO200142463-A1.
XX
PD   14-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-US30166.
XX
PR   07-DEC-1999;   99US-0169367.
PR   07-DEC-1999;   99US-0169381.
PR   07-DEC-1999;   99US-0169412.
PR   23-MAR-2000; 2000US-0191430.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Lu J,  Witcher DR;
XX
DR   WPI; 2001-381684/40.
XX
PT   New FLINT polypeptide for treating and/or preventing acute lung injury,
PT   acute respiratory distress syndrome, ulcerative colitis, and
PT   graft-versus-host disease, comprises O-linked or N-linked
PT   oligosaccharides -
XX
PS   Disclosure; Page -; 60pp; English.
XX
CC   The present sequence is human mature fas ligand inhibitory protein
CC   (FLINT) variant, R218E. FLINT, a homologue of tumour necrosis factor
CC   receptor protein (TNFR), binds fas ligand (FasL) and thereby preventing
CC   the interaction of FasL with fas. FLINT comprising O-linked or N-linked
CC   oligosaccharides is useful for preventing or treating acute lung injury
CC   (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,
CC   chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),
CC   to facilitate organ preservation for transplantation and to inhibit T
CC   lymphocyte activation. FLINT is useful for treating and/or preventing
CC   diseases such as rheumatoid arthritis, fibroproliferative lung disease,
CC   fibrotic lung disease, acute lung injury, human immunodeficiency virus
CC   (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-
CC   host disease, cutaneous inflammation, vascular leak syndrome,
CC   Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent
CC   diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,
CC   Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as
CC   psoriasis, Down's syndrome, and multiple sclerosis.
CC   Note: The present sequence is not shown in the specification, but is
CC   derived from the mature FLINT sequence shown as SEQ ID NO:1 (AAE03567)
CC   in sequence listing of the specification.
XX
SQ   Sequence   271 AA;

  Query Match             90.9%;  Score 1486;  DB 22;  Length 271;
  Best Local Similarity   99.6%;  Pred. No. 6.6e-110;
  Matches  270;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPEAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 54
AAE14582
ID   AAE14582 standard; Protein; 271 AA.
XX
AC   AAE14582;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human protease-resistant mature FLINT analogue (R218E).
XX
KW   FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW   organ failure; liver; kidney; pancreas; inflammatory disease;
KW   neutrophil; sepsis; acute respiratory distress syndrome;
KW   acute lung injury; systemic inflammatory response syndrome; SIRS;
KW   multiple organ dysfunction; MODS; human; protease-resistant;
KW   mutant; mutein.
XX
OS   Homo sapiens.
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 218
FT                   /note= "Wild-type Arg is replaced with Glu"
XX
PN   WO200209668-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-US21105.
XX
PR   02-AUG-2000; 2000US-222476P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Witcher DR;
XX
DR   WPI; 2002-206149/26.
XX
PT   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT   useful for treating e.g. sepsis or respiratory distress syndrome,
PT   involves pulmonary administration of a therapeutic amount of the FLINT
PT   or FLINT analog -
XX
PS   Disclosure; Page -; 35pp; English.
XX
CC   The invention relates to a new method of administering FLINT
CC   (FAS ligand inhibitory protein) or FLINT analogue that involves pulmonary
CC   administration of a therapeutic amount of the FLINT or FLINT analogue.
CC   The method enables systemic absorption of FLINT through lungs and
CC   significantly reduces or eliminates the need for administering FLINT by
CC   injection or other routes of administration. The method is useful in
CC   treating disorders related to enhanced apoptosis (e.g. organ failure
CC   in liver, kidneys and pancreas) and inflammatory diseases associated with
CC   neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC   acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC   multiple organ dysfunction (MODS)). The method minimises the pain
CC   and discomfort of injection methods. The present sequence is human
CC   protease-resistant mature FLINT analogue (R218E).
CC   Note: The present sequence is not shown in the specification, but
CC   is derived from the mature FLINT protein sequence (SEQ ID NO:1) shown in
CC   Sequence Listing (AAE14578).
XX
SQ   Sequence   271 AA;

  Query Match             90.9%;  Score 1486;  DB 23;  Length 271;
  Best Local Similarity   99.6%;  Pred. No. 6.6e-110;
  Matches  270;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPEAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 55
AAY96599
ID   AAY96599 standard; Protein; 271 AA.
XX
AC   AAY96599;
XX
DT   26-SEP-2000  (first entry)
XX
DE   Human mature FLINT.
XX
KW   FLINT; osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNFR;
KW   FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
KW   anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
KW   anti-inflammatory; antibacterial; immunosuppressive.
XX
OS   Homo sapiens.
XX
PN   WO200037094-A2.
XX
PD   29-JUN-2000.
XX
PF   21-DEC-1999;   99WO-US30734.
XX
PR   22-DEC-1998;   98US-0113407.
PR   30-MAR-1999;   99WO-US06797.
PR   20-OCT-1999;   99US-0172239.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Cohen FJ,  Posada JA,  Wierda D;
XX
DR   WPI; 2000-475441/41.
DR   N-PSDB; AAA51078.
XX
PT   Use of mature FLINT for treating e.g. acute respiratory distress
PT   syndrome, ulcerative colitis or ischemic injury during organ
PT   transplantation
XX
PS   Example 1; Fig 4A-B; 125pp; English.
XX
CC   Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis
CC   factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
CC   prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
CC   mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
CC   treating acute respiratory distress syndrome, treating or inhibiting
CC   ulcerative colitis, inhibiting ischemic injury during organ
CC   transplantation or for organ preservation during transplantation. mFLINT
CC   can also be used to treat acute liver failure, inflammation of the liver,
CC   abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
CC   inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
CC   damage to a cardiac myocyte resulting from abnormal myocardial ischaemia,
CC   Type I diabetes, cancer, damage to an innocent bystander tissue induced
CC   by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
CC   myelodysplastic syndromes and pancytopenic conditions.
XX
SQ   Sequence   271 AA;

  Query Match             90.9%;  Score 1485;  DB 21;  Length 271;
  Best Local Similarity   99.6%;  Pred. No. 8e-110;
  Matches  270;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
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Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWAPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 56
AAE14583
ID   AAE14583 standard; Protein; 271 AA.
XX
AC   AAE14583;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human protease-resistant mature FLINT analogue (T216P).
XX
KW   FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW   organ failure; liver; kidney; pancreas; inflammatory disease;
KW   neutrophil; sepsis; acute respiratory distress syndrome;
KW   acute lung injury; systemic inflammatory response syndrome; SIRS;
KW   multiple organ dysfunction; MODS; human; protease-resistant;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 216
FT                   /note= "Wild-type Thr is replaced with Pro"
XX
PN   WO200209668-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-US21105.
XX
PR   02-AUG-2000; 2000US-222476P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Witcher DR;
XX
DR   WPI; 2002-206149/26.
XX
PT   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT   useful for treating e.g. sepsis or respiratory distress syndrome,
PT   involves pulmonary administration of a therapeutic amount of the FLINT
PT   or FLINT analog -
XX
PS   Disclosure; Page -; 35pp; English.
XX
CC   The invention relates to a new method of administering FLINT
CC   (FAS ligand inhibitory protein) or FLINT analogue that involves pulmonary
CC   administration of a therapeutic amount of the FLINT or FLINT analogue.
CC   The method enables systemic absorption of FLINT through lungs and
CC   significantly reduces or eliminates the need for administering FLINT by
CC   injection or other routes of administration. The method is useful in
CC   treating disorders related to enhanced apoptosis (e.g. organ failure
CC   in liver, kidneys and pancreas) and inflammatory diseases associated with
CC   neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC   acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC   multiple organ dysfunction (MODS)). The method minimises the pain
CC   and discomfort of injection methods. The present sequence is human
CC   protease-resistant mature FLINT analogue (T216P).
CC   Note: The present sequence is not shown in the specification, but
CC   is derived from the mature FLINT protein sequence (SEQ ID NO:1) shown in
CC   Sequence Listing (AAE14578).
XX
SQ   Sequence   271 AA;

  Query Match           90.9%;  Score 1485;  DB 23;  Length 271;
  Best Local Similarity 99.6%;  Pred. No. 8e-110;
  Matches  270;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPPPRAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 57
AAE14584
ID   AAE14584 standard; Protein; 271 AA.
XX
AC   AAE14584;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human protease-resistant mature FLINT analogue (R218A).
XX
KW   FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW   organ failure; liver; kidney; pancreas; inflammatory disease;
KW   neutrophil; sepsis; acute respiratory distress syndrome;
KW   acute lung injury; systemic inflammatory response syndrome; SIRS;
KW   multiple organ dysfunction; MODS; human; protease-resistant;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 218
FT                   /note= "Wild-type Arg is replaced with Ala"
XX
PN   WO200209668-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-US21105.
XX
PR   02-AUG-2000; 2000US-222476P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Witcher DR;
XX
DR   WPI; 2002-206149/26.
XX
PT   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT   useful for treating e.g. sepsis or respiratory distress syndrome,
PT   involves pulmonary administration of a therapeutic amount of the FLINT
PT   or FLINT analog -
XX
PS   Disclosure; Page -; 35pp; English.
XX
CC   The invention relates to a new method of administering FLINT
CC   (FAS ligand inhibitory protein) or FLINT analogue that involves pulmonary
CC   administration of a therapeutic amount of the FLINT or FLINT analogue.
CC   The method enables systemic absorption of FLINT through lungs and
CC   significantly reduces or eliminates the need for administering FLINT by
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CC   injection or other routes of administration. The method is useful in
CC   treating disorders related to enhanced apoptosis (e.g. organ failure
CC   in liver, kidneys and pancreas) and inflammatory diseases associated with
CC   neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC   acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC   multiple organ dysfunction (MODS)). The method minimises the pain
CC   and discomfort of injection methods. The present sequence is human
CC   protease-resistant mature FLINT analogue (R218A).
CC   Note: The present sequence is not shown in the specification, but
CC   is derived from the mature FLINT protein sequence (SEQ ID NO:1) shown in
CC   Sequence Listing (AAE14578).
XX
SQ   Sequence   271 AA;

  Query Match             90.9%;  Score 1485;  DB 23;  Length 271;
  Best Local Similarity   99.6%;  Pred. No. 8e-110;
  Matches  270;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPAAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 58
AAE14586
ID   AAE14586 standard; Protein; 271 AA.
XX
AC   AAE14586;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human protease-resistant mature FLINT analogue (R218S).
XX
KW   FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW   organ failure; liver; kidney; pancreas; inflammatory disease;
KW   neutrophil; sepsis; acute respiratory distress syndrome;
KW   acute lung injury; systemic inflammatory response syndrome; SIRS;
KW   multiple organ dysfunction; MODS; human; protease-resistant;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 218
FT                   /note= "Wild-type Arg is replaced with Ser"
XX
PN   WO200209668-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-US21105.
XX
PR   02-AUG-2000; 2000US-222476P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Witcher DR;
XX
DR   WPI; 2002-206149/26.
XX
PT   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT   useful for treating e.g. sepsis or respiratory distress syndrome,
PT   involves pulmonary administration of a therapeutic amount of the FLINT
PT   or FLINT analog -
XX
PS   Disclosure; Page -; 35pp; English.
XX
CC   The invention relates to a new method of administering FLINT
CC   (FAS ligand inhibitory protein) or FLINT analogue that involves pulmonary
CC   administration of a therapeutic amount of the FLINT or FLINT analogue.
CC   The method enables systemic absorption of FLINT through lungs and
CC   significantly reduces or eliminates the need for administering FLINT by
CC   injection or other routes of administration. The method is useful in
CC   treating disorders related to enhanced apoptosis (e.g. organ failure
CC   in liver, kidneys and pancreas) and inflammatory diseases associated with
CC   neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC   acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC   multiple organ dysfunction (MODS)). The method minimises the pain
CC   and discomfort of injection methods. The present sequence is human
CC   protease-resistant mature FLINT analogue (R218S).
CC   Note: The present sequence is not shown in the specification, but
CC   is derived from the mature FLINT protein sequence (SEQ ID NO:1) shown in
CC   Sequence Listing (AAE14578).
XX
SQ   Sequence   271 AA;

  Query Match             90.9%;  Score 1485;  DB 23;  Length 271;
  Best Local Similarity   99.6%;  Pred. No. 8e-110;
  Matches  270;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPSAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 59
AAE14590
ID   AAE14590 standard; Protein; 271 AA.
XX
AC   AAE14590;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human protease-resistant mature FLINT analogue (T216P).
XX
KW   FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW   organ failure; liver; kidney; pancreas; inflammatory disease;
KW   neutrophil; sepsis; acute respiratory distress syndrome;
KW   acute lung injury; systemic inflammatory response syndrome; SIRS;
KW   multiple organ dysfunction; MODS; human; protease-resistant;
KW   mutant; mutein.
XX
OS   Homo sapiens.
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 216
FT                   /note= "Wild-type Thr is replaced with Pro"
XX
PN   WO200209668-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-US21105.
XX
PR   02-AUG-2000; 2000US-222476P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Witcher DR;
XX
DR   WPI; 2002-206149/26.
XX
PT   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT   useful for treating e.g. sepsis or respiratory distress syndrome,
PT   involves pulmonary administration of a therapeutic amount of the FLINT
PT   or FLINT analog -
XX
PS   Disclosure; Page -; 35pp; English.
XX
CC   The invention relates to a new method of administering FLINT
CC   (FAS ligand inhibitory protein) or FLINT analogue that involves pulmonary
CC   administration of a therapeutic amount of the FLINT or FLINT analogue.
CC   The method enables systemic absorption of FLINT through lungs and
CC   significantly reduces or eliminates the need for administering FLINT by
CC   injection or other routes of administration. The method is useful in
CC   treating disorders related to enhanced apoptosis (e.g. organ failure
CC   in liver, kidneys and pancreas) and inflammatory diseases associated with
CC   neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC   acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC   multiple organ dysfunction (MODS)). The method minimises the pain
CC   and discomfort of injection methods. The present sequence is human
CC   protease-resistant mature FLINT analogue (T216P).
CC   Note: The present sequence is not shown in the specification, but
CC   is derived from the mature FLINT protein sequence (SEQ ID NO:1) shown in
CC   Sequence Listing (AAE14578).
XX
SQ   Sequence   271 AA;

  Query Match             90.9%;  Score 1485;  DB 23;  Length 271;
  Best Local Similarity   99.6%;  Pred. No. 8e-110;
  Matches  270;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPPPRAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 60
AAE14585
ID   AAE14585 standard; Protein; 271 AA.
XX
AC   AAE14585;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human protease-resistant mature FLINT analogue (R218G).
XX
KW   FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW   organ failure; liver; kidney; pancreas; inflammatory disease;
KW   neutrophil; sepsis; acute respiratory distress syndrome;
KW   acute lung injury; systemic inflammatory response syndrome; SIRS;
KW   multiple organ dysfunction; MODS; human; protease-resistant;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 218
FT                   /note= "Wild-type Arg is replaced with Gly"
XX
PN   WO200209668-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-US21105.
XX
PR   02-AUG-2000; 2000US-222476P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Witcher DR;
XX
DR   WPI; 2002-206149/26.
XX
PT   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT   useful for treating e.g. sepsis or respiratory distress syndrome,
PT   involves pulmonary administration of a therapeutic amount of the FLINT
PT   or FLINT analog -
XX
PS   Disclosure; Page -; 35pp; English.
XX
CC   The invention relates to a new method of administering FLINT
CC   (FAS ligand inhibitory protein) or FLINT analogue that involves pulmonary
CC   administration of a therapeutic amount of the FLINT or FLINT analogue.
CC   The method enables systemic absorption of FLINT through lungs and
CC   significantly reduces or eliminates the need for administering FLINT by
CC   injection or other routes of administration. The method is useful in
CC   treating disorders related to enhanced apoptosis (e.g. organ failure
CC   in liver, kidneys and pancreas) and inflammatory diseases associated with
CC   neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC   acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC   multiple organ dysfunction (MODS)). The method minimises the pain
CC   and discomfort of injection methods. The present sequence is human
CC   protease-resistant mature FLINT analogue (R218G).
CC   Note: The present sequence is not shown in the specification, but
CC   is derived from the mature FLINT protein sequence (SEQ ID NO:1) shown in
CC   Sequence Listing (AAE14578).
XX
SQ   Sequence   271 AA;

  Query Match             90.8%;  Score 1484;  DB 23;  Length 271;
  Best Local Similarity   99.6%;  Pred. No. 9.6e-110;
  Matches  270;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
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Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPGAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 61
AAE14588
ID   AAE14588 standard; Protein; 271 AA.
XX
AC   AAE14588;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human protease-resistant mature FLINT analogue (R218Y).
XX
KW   FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW   organ failure; liver; kidney; pancreas; inflammatory disease;
KW   neutrophil; sepsis; acute respiratory distress syndrome;
KW   acute lung injury; systemic inflammatory response syndrome; SIRS;
KW   multiple organ dysfunction; MODS; human; protease-resistant;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 218
FT                   /note= "Wild-type Arg is replaced with Tyr"
XX
PN   WO200209668-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-US21105.
XX
PR   02-AUG-2000; 2000US-222476P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Witcher DR;
XX
DR   WPI; 2002-206149/26.
XX
PT   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT   useful for treating e.g. sepsis or respiratory distress syndrome,
PT   involves pulmonary administration of a therapeutic amount of the FLINT
PT   or FLINT analog -
XX
PS   Disclosure; Page -; 35pp; English.
XX
CC   The invention relates to a new method of administering FLINT
CC   (FAS ligand inhibitory protein) or FLINT analogue that involves pulmonary
CC   administration of a therapeutic amount of the FLINT or FLINT analogue.
CC   The method enables systemic absorption of FLINT through lungs and
CC   significantly reduces or eliminates the need for administering FLINT by
CC   injection or other routes of administration. The method is useful in
CC   treating disorders related to enhanced apoptosis (e.g. organ failure
CC   in liver, kidneys and pancreas) and inflammatory diseases associated with
CC   neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC   acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC   multiple organ dysfunction (MODS)). The method minimises the pain
CC   and discomfort of injection methods. The present sequence is human
CC   protease-resistant mature FLINT analogue (R218Y).
CC   Note: The present sequence is not shown in the specification, but
CC   is derived from the mature FLINT protein sequence (SEQ ID NO:1) shown in
CC   Sequence Listing (AAE14578).
XX
SQ   Sequence   271 AA;

  Query Match             90.8%;  Score 1484;  DB 23;  Length 271;
  Best Local Similarity   99.6%;  Pred. No. 9.6e-110;
  Matches  270;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPYAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 62
AAE14587
ID   AAE14587 standard; Protein; 271 AA.
XX
AC   AAE14587;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human protease-resistant mature FLINT analogue (R218V).
XX
KW   FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW   organ failure; liver; kidney; pancreas; inflammatory disease;
KW   neutrophil; sepsis; acute respiratory distress syndrome;
KW   acute lung injury; systemic inflammatory response syndrome; SIRS;
KW   multiple organ dysfunction; MODS; human; protease-resistant;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 218
FT                   /note= "Wild-type Arg is replaced with Val"
XX
PN   WO200209668-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-US21105.
XX
PR   02-AUG-2000; 2000US-222476P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Witcher DR;
XX
DR   WPI; 2002-206149/26.
XX
PT   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT   useful for treating e.g. sepsis or respiratory distress syndrome,
PT   involves pulmonary administration of a therapeutic amount of the FLINT
PT   or FLINT analog -
XX
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PS   Disclosure; Page -; 35pp; English.
XX
CC   The invention relates to a new method of administering FLINT
CC   (FAS ligand inhibitory protein) or FLINT analogue that involves pulmonary
CC   administration of a therapeutic amount of the FLINT or FLINT analogue.
CC   The method enables systemic absorption of FLINT through lungs and
CC   significantly reduces or eliminates the need for administering FLINT by
CC   injection or other routes of administration. The method is useful in
CC   treating disorders related to enhanced apoptosis (e.g. organ failure
CC   in liver, kidneys and pancreas) and inflammatory diseases associated with
CC   neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC   acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC   multiple organ dysfunction (MODS)). The method minimises the pain
CC   and discomfort of injection methods. The present sequence is human
CC   protease-resistant mature FLINT analogue (R218V).
CC   Note: The present sequence is not shown in the specification, but
CC   is derived from the mature FLINT protein sequence (SEQ ID NO:1) shown in
CC   Sequence Listing (AAE14578).
XX
SQ   Sequence   271 AA;

  Query Match             90.8%;  Score 1483;  DB 23;  Length 271;
  Best Local Similarity   99.6%;  Pred. No. 1.1e-109;
  Matches  270;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPVAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 63
AAB19708
ID   AAB19708 standard; Protein; 271 AA.
XX
AC   AAB19708;
XX
DT   05-FEB-2001  (first entry)
XX
DE   Protease-resistant FLINT analogue, T216P, R218Q substitution.
XX
KW   FLINT; FAS ligand inhibitory protein; human; protease resistant;
KW   acute lung injury; acute respiratory distress syndrome;
KW   chronic obstructive pulmonary disease; pulmonary fibrosis;
KW   ulcerative colitis; therapy; organ transplantation; substitution;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 216
FT                   /note= "Wild-type Thr substituted by Pro"
FT   Misc-difference 218
FT                   /note= "Wild-type Arg substituted by Gln"
XX
PN   WO200058466-A2.
XX
PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-US06418.
XX
PR   30-MAR-1999;   99US-0126839.
PR   21-JUN-1999;   99US-0140073.
PR   04-AUG-1999;   99US-0147071.
PR   20-OCT-1999;   99US-0160524.
PR   21-OCT-1999;   99US-0160669.
PR   20-DEC-1999;   99US-0172744.
PR   26-JAN-2000; 2000US-0178184.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Rathnachalam R,  Witcher DR;
XX
DR   WPI; 2000-664925/64.
XX
PT   Novel protease resistant FAS ligand inhibitory protein analogues
PT   resistant to in vivo or in vitro proteolysis at amino acid position 218
PT   of the mature protein, useful for treating autoimmune diseases -
XX
PS   Claim 15; Page -; 100pp; English.
XX
CC   Novel human FLINT analogues are resistant to proteolysis at
CC   position 218 of the wild-type protein (see AAB19705).  The present
CC   sequence is a specific example of a protease-resistant FLINT
CC   analogue in which the Thr residue at position 216 has been
CC   substituted by an Asn residue, and the Arg residue at position
CC   218 has been substituted by a Gln residue.  The FLINT analogue can
CC   be obtained by mutagenesis of template FLINT cDNA (see AAA88730) and
CC   expressed in recombinant host cells.  It is used to prevent or
CC   treat acute lung injury, acute respiratory stress syndrome,
CC   ulcerative colitis, chronic obstructive pulmonary disease, and
CC   pulmonary fibrosis.  It is also used to inhibit T lymphocyte
CC   activation, to inhibit ischaemic injury during organ
CC   transplantation, and as a component of a liquid medium for
CC   infusion and preservation of organs (claimed).  Resistance to
CC   proteolytic cleavage greatly increases in vivo half-life.
CC   Note: The present sequence is not shown in the specification but is
CC   derived from the human FLINT mature protein sequence given in
CC   the Sequence Listing (see AAB19705).
XX
SQ   Sequence   271 AA;

  Query Match             90.6%;  Score 1481;  DB 21;  Length 271;
  Best Local Similarity   99.3%;  Pred. No. 1.7e-109;
  Matches  269;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              |||||||||||||||||||||||||||||||| |:||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPPPQAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 64
AAE14589
ID   AAE14589 standard; Protein; 271 AA.
```

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XX
AC   AAE14589;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human protease-resistant mature FLINT analogue (P217Y).
XX
KW   FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;
KW   organ failure; liver; kidney; pancreas; inflammatory disease;
KW   neutrophil; sepsis; acute respiratory distress syndrome;
KW   acute lung injury; systemic inflammatory response syndrome; SIRS;
KW   multiple organ dysfunction; MODS; human; protease-resistant;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 217
FT                   /note= "Wild-type Pro is replaced with Tyr"
XX
PN   WO200209668-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-US21105.
XX
PR   02-AUG-2000; 2000US-222476P.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Witcher DR;
XX
DR   WPI; 2002-206149/26.
XX
PT   Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,
PT   useful for treating e.g. sepsis or respiratory distress syndrome,
PT   involves pulmonary administration of a therapeutic amount of the FLINT
PT   or FLINT analog -
XX
PS   Disclosure; Page -; 35pp; English.
XX
CC   The invention relates to a new method of administering FLINT
CC   (FAS ligand inhibitory protein) or FLINT analogue that involves pulmonary
CC   administration of a therapeutic amount of the FLINT or FLINT analogue.
CC   The method enables systemic absorption of FLINT through lungs and
CC   significantly reduces or eliminates the need for administering FLINT by
CC   injection or other routes of administration. The method is useful in
CC   treating disorders related to enhanced apoptosis (e.g. organ failure
CC   in liver, kidneys and pancreas) and inflammatory diseases associated with
CC   neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
CC   acute lung injury, systemic inflammatory response syndrome (SIRS) and
CC   multiple organ dysfunction (MODS)). The method minimises the pain
CC   and discomfort of injection methods. The present sequence is human
CC   protease-resistant mature FLINT analogue (P217Y).
CC   Note: The present sequence is not shown in the specification, but
CC   is derived from the mature FLINT protein sequence (SEQ ID NO:1) shown in
CC   Sequence Listing (AAE14578).
XX
SQ   Sequence   271 AA;

  Query Match             90.6%;  Score 1481;  DB 23;  Length 271;
  Best Local Similarity   99.6%;  Pred. No. 1.7e-109;
  Matches  270;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTYRAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 65
AAB19706
ID   AAB19706 standard; Protein; 271 AA.
XX
AC   AAB19706;
XX
DT   05-FEB-2001  (first entry)
XX
DE   Protease-resistant FLINT analogue, R34N, D36T, R218Q substitution.
XX
KW   FLINT; FAS ligand inhibitory protein; human; protease resistant;
KW   acute lung injury; acute respiratory distress syndrome;
KW   chronic obstructive pulmonary disease; pulmonary fibrosis;
KW   ulcerative colitis; therapy; organ transplantation; substitution;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 34
FT                   /note= "Wild-type Arg substituted by Asn"
FT   Misc-difference 36
FT                   /note= "Wild-type Asp substituted by Thr"
FT   Misc-difference 218
FT                   /note= "Wild-type Arg substituted by Gln"
XX
PN   WO200058466-A2.
XX
PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-US06418.
XX
PR   30-MAR-1999;   99US-0126839.
PR   21-JUN-1999;   99US-0140073.
PR   04-AUG-1999;   99US-0147071.
PR   20-OCT-1999;   99US-0160524.
PR   21-OCT-1999;   99US-0160669.
PR   20-DEC-1999;   99US-0172744.
PR   26-JAN-2000; 2000US-0178184.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Rathnachalam R,  Witcher DR;
XX
DR   WPI; 2000-664925/64.
XX
PT   Novel protease resistant FAS ligand inhibitory protein analogues
PT   resistant to in vivo or in vitro proteolysis at amino acid position 218
PT   of the mature protein, useful for treating autoimmune diseases  -
XX
PS   Claim 13; Page -; 100pp; English.
XX
CC   Novel human FLINT analogues are resistant to proteolysis at
CC   position 218 of the wild-type protein (see AAB19705).  The present
CC   sequence is a specific example of a protease-resistant FLINT
CC   analogue in which the Arg residue at position 34 has been
CC   substituted by an Asn residue, the Asp residue at position 36 has
CC   been substituted by a Thr residue, and the Arg residue at position
CC   218 has been substituted by a Gln residue.  The FLINT analogue can
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CC   be obtained by mutagenesis of template FLINT cDNA (see AAA88730) and
CC   expressed in recombinant host cells.  It is used to prevent or
CC   treat acute lung injury, acute respiratory stress syndrome,
CC   ulcerative colitis, chronic obstructive pulmonary disease, and
CC   pulmonary fibrosis.  It is also used to inhibit T lymphocyte
CC   activation, to inhibit ischaemic injury during organ
CC   transplantation, and as a component of a liquid medium for
CC   infusion and preservation of organs (claimed).  Resistance to
CC   proteolytic cleavage greatly increases in vivo half-life.
CC   Note: The present sequence is not shown in the specification but is
CC   derived from the human FLINT mature protein sequence given in
CC   the Sequence Listing (see AAB19705).
XX
SQ   Sequence   271 AA;

  Query Match             90.3%;  Score 1475;  DB 21;  Length 271;
  Best Local Similarity   98.9%;  Pred. No. 4.9e-109;
  Matches  268;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              |||||||||||||||||||||||||||||||| | ||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCNRTSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              ||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPQAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 66
AAB68046
ID   AAB68046 standard; Protein; 271 AA.
XX
AC   AAB68046;
XX
DT   29-JUN-2001  (first entry)
XX
DE   Amino acid sequence of a modified human mature FLINT polypeptide.
XX
KW   FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;
KW   Fas ligand; acute liver failure; cerebral ischemia; apoptosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 34
FT                   /note= "Arg replaced by Asn"
FT   Misc-difference 36
FT                   /note= "Asp replaced by Thr"
FT   Misc-difference 194
FT                   /note= "Asp replaced by Asn"
FT   Misc-difference 196
FT                   /note= "Ser replaced by Thr"
XX
PN   WO200118055-A1.
XX
PD   15-MAR-2001.
XX
PF   31-AUG-2000; 2000WO-US20807.
XX
PR   10-SEP-1999;   99US-0153339.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Atkinson PR,  Tian Y,  Witcher DR;
XX
DR   WPI; 2001-273382/28.
XX
PT   Compositions comprising a divalent metal cation and a FAS Ligand
PT   Inhibitory Protein (FLINT), for reducing or inducing aggregation of
PT   FLINT and for treating diseases involving FasL/Fas and/or
PT   LIGHT/LT-beta-R receptor interactions
XX
PS   Example 1; Page -; 44pp; English.
XX
CC   The present sequence represents a modified mature FLINT (FAS Ligand
CC   Inhibitory Protein) polypeptide. The specification describers a
CC   composition comprising a divalent metal cation and FLINT protein. The
CC   composition is used either for reducing, reversing or eliminating
CC   aggregation and precipitation of FLINT or for inducing oligomerisation
CC   or aggregation of FLINT molecules. They can be used for purifying FLINT
CC   and/or maintaining FLINT in solution. The compositions are used to treat
CC   and/or prevent disorders associated with the binding of Fas to FasL
CC   and/or LIGHT to the LTbetaR and/or TR2/HVEM receptors. Uses include the
CC   treatment of acute liver failure and cerebral ischemia and the prevention
CC   of apoptosis.
CC   note: this sequence does not appear in the specification; it was created
CC   using information provided.
XX
SQ   Sequence   271 AA;

  Query Match             90.0%;  Score 1471;  DB 22;  Length 271;
  Best Local Similarity   98.5%;  Pred. No. 1e-108;
  Matches  267;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              |||||||||||||||||||||||||||||||| | ||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCNRTSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              |||||||||||||:|:||||||||||||||||||||||||||||||||||||||||||||
Db        181 ECERAVIDFVAFQNITIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 67
AAB19707
ID   AAB19707 standard; Protein; 271 AA.
XX
AC   AAB19707;
XX
DT   05-FEB-2001  (first entry)
XX
DE   Protease-resistant FLINT analogue R34N, D36T, D194T, S196T, R218Q.
XX
KW   FLINT; FAS ligand inhibitory protein; human; protease resistant;
KW   acute lung injury; acute respiratory distress syndrome;
KW   chronic obstructive pulmonary disease; pulmonary fibrosis;
KW   ulcerative colitis; therapy; organ transplantation; substitution;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
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FH   Key             Location/Qualifiers
FT   Misc-difference 34
FT                   /note= "Wild-type Arg substituted by Asn"
FT   Misc-difference 194
FT                   /note= "Wild-type Asp substituted by Asn"
FT   Misc-difference 196
FT                   /note= "Wild-type Ser substituted by Thr"
FT   Misc-difference 36
FT                   /note= "Wild-type Asp substituted by Thr"
FT   Misc-difference 218
FT                   /note= "Wild-type Arg substituted by Gln"
XX
PN   WO200058466-A2.
XX
PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-US06418.
XX
PR   30-MAR-1999;   99US-0126839.
PR   21-JUN-1999;   99US-0140073.
PR   04-AUG-1999;   99US-0147071.
PR   20-OCT-1999;   99US-0160524.
PR   21-OCT-1999;   99US-0160669.
PR   20-DEC-1999;   99US-0172744.
PR   26-JAN-2000; 2000US-0178184.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Micanovic R,  Rathnachalam R,  Witcher DR;
XX
DR   WPI; 2000-664925/64.
XX
PT   Novel protease resistant FAS ligand inhibitory protein analogues
PT   resistant to in vivo or in vitro proteolysis at amino acid position 218
PT   of the mature protein, useful for treating autoimmune diseases  -
XX
PS   Claim 14; Page -; 100pp; English.
XX
CC   Novel human FLINT analogues are resistant to proteolysis at
CC   position 218 of the wild-type protein (see AAB19705).  The present
CC   sequence is a specific example of a protease-resistant FLINT
CC   analogue in which the Arg residue at position 34 has been
CC   substituted by an Asn residue, the Asp residue at position 36 has
CC   been substituted by a Thr residue, the Asp residue at position 194
CC   has been substituted by an Asn residue, the Ser residue at
CC   position 196 has been substituted by a Thr residue, and the Arg
CC   residue at position 218 has been substituted by a Gln residue.
CC   The FLINT analogue can be obtained by mutagenesis of template
CC   FLINT cDNA (see AAA88730) and expressed in recombinant host cells.
CC   It is used to prevent or treat acute lung injury, acute respiratory
CC   stress syndrome, ulcerative colitis, chronic obstructive pulmonary
CC   disease and pulmonary fibrosis.  It is also used to inhibit T
CC   lymphocyte activation, to inhibit ischaemic injury during organ
CC   transplantation, and as a component of a liquid medium for
CC   infusion and preservation of organs (claimed).  Resistance to
CC   proteolytic cleavage greatly increases in vivo half-life.
CC   Note: The present sequence is not shown in the specification but is
CC   derived from the human FLINT mature protein sequence given in
CC   the Sequence Listing (see AAB19705).
XX
SQ   Sequence   271 AA;

  Query Match             89.8%;  Score 1467;  DB 21;  Length 271;
  Best Local Similarity   98.2%;  Pred. No. 2.1e-108;
  Matches  266;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCNRTSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120

Qy        150 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPGAE 180

Qy        210 ECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGAQD 269
              |||||||||||||:|:||||||||||||||||||||:||||||||||||||||||||||
Db        181 ECERAVIDFVAFQNITIKRLQRLLQALEAPEGWGPTPQAGRAALQLKLRRRLTELLGAQD 240

Qy        270 GALLVRLLQALRVARMPGLERSVRERFLPVH 300
              |||||||||||||||||||||||||||||||
Db        241 GALLVRLLQALRVARMPGLERSVRERFLPVH 271


RESULT 68
AAY42185
ID   AAY42185 standard; Protein; 273 AA.
XX
AC   AAY42185;
XX
DT   17-DEC-1999  (first entry)
XX
DE   Human mFLINT #2 protein sequence.
XX
KW   Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
KW   apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW   sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW   reperfusion-associated injury; aplastic anaemia; differentiation;
KW   growth; myelodysplastic syndrome; pancytopenic condition;
KW   myocardial ischaemia.
XX
OS   Homo sapiens.
XX
PN   WO9950413-A2.
XX
PD   07-OCT-1999.
XX
PF   30-MAR-1999;   99WO-US06797.
XX
PR   30-MAR-1998;   98US-0079856.
PR   20-MAY-1998;   98US-0086074.
PR   09-SEP-1998;   98US-0099643.
PR   17-DEC-1998;   98US-0112577.
PR   18-DEC-1998;   98US-0112703.
PR   18-DEC-1998;   98US-0112933.
PR   22-DEC-1998;   98US-0113407.
XX
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Bumol TF,  Dou S,  Glasebrook AL,  Gould KE,  Hale JE,  Heuer JG;
PI   Hui KY,  Kharitonenkov A,  Mizrahi J,  Na S,  Noblitt TW,  Reidy CA;
PI   Song HY,  Wang J,  Wu X,  Zuckerman SH;
XX
DR   WPI; 1999-591319/50.
DR   N-PSDB; AAZ25378.
XX
PT   Use of mature FLINT for treating acute liver failure, inflammation,
PT   cancer, and diabetes  - by prevention of FasL-Fas mediated apoptotic
PT   and proinflammatory activity
XX
PS   Example 2; Fig 4; 99pp; English.
XX
CC   The present invention describes therapeutic applications of mature FLINT
CC   (mFLINT) for use in the treatment of acute liver failure. Mature FLINT
CC   (mFLINT), which is a member of the tumour necrosis factor receptor
CC   superfamily, is used for treating acute liver failure, inflammation of
CC   the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
CC   with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
CC   injury or disorder such as hypercoagulation (including use with
CC   thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
CC   or disorder, Type I diabetes, cancer, cell damage or damage to an
CC   innocent bystander tissue that is induced by a chemotherapeutic agent or
CC   therapeutic irradiation, treating haematopoietic progenitor cells that
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CC   have been exposed to therapeutic radiation or chemotherapy, aplastic
CC   anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is
CC   also used for promoting the growth or differentiation of a haematopoietic
CC   progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
CC   resulting from abnormal myocardial ischaemia. The present sequence
CC   represents human mFLINT.
XX
SQ   Sequence   273 AA;

  Query Match             89.8%;  Score 1467;  DB 20;  Length 273;
  Best Local Similarity   98.5%;  Pred. No. 2.1e-108;
  Matches  269;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    1;

Qy         30 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAETPTYPWRDAETGERLVCAQCPPGTFVQRPCRRDSPTTCGPCPPRHYTQFWNYLERCR 60

Qy         90 YCNVLCGEREEEARACHATHNRA--CRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQN 147
              |||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db         61 YCNVLCGEREEEARACHATHNRACRCRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQN 120

Qy        148 TQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPG 207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRVPG 180

Qy        208 AEECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELLGA 267
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        181 AEECERAVIDFVAFQDISIKRLQRLLQALEAPEGWAPTPRAGRAALQLKLRRRLTELLGA 240

Qy        268 QDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              |||||||||||||||||||||||||||||| |
Db        241 QDGALLVRLLQALRVARMPGLERSVRERFLPWH 273


RESULT 69
AAY28449
ID   AAY28449 standard; Protein; 245 AA.
XX
AC   AAY28449;
XX
DT   29-SEP-1999  (first entry)
XX
DE   A human tumour necrosis factor-R2-like proteins (TR2P)-1.
XX
KW   Human tumour necrosis factor-R2-like protein; TR2P; achondroplasia;
KW   osteoporosis; developmental disorder; Cushing's syndrome;
KW   muscular dystrophy; epilepsy; hereditary neuropathy;
KW   Charcot-Marie-Tooth disease; neurofibromatosis; hypothyroidism;
KW   hydrocephalus; seizure disorder; cerebral palsy; spinal bifida;
KW   congenital glaucoma; cataract; sensorineural hearing loss;
KW   reproductive disorder; infertility; ovulatory defect; endometriosis;
KW   autoimmune disorder; ectopic pregnancy; teratogenesis; spermatogenesis;
KW   immunological disorder; AIDS; Addison's disease; allergy; bronchitis;
KW   atherssclerosis; diabetes mellitus; Chron's disease; lupus;
KW   irritable bowel syndrome; multiple sclerosis; infection;
KW   neoplastic disorder; adenocarcinoma; leukaemia; lymphoma; melanoma;
KW   myeloma; sarcoma.
XX
OS   Homo sapiens.
XX
PN   WO9931128-A2.
XX
PD   24-JUN-1999.
XX
PF   02-DEC-1998;   98WO-US25649.
XX
PR   16-DEC-1997;   97US-0991945.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Au-Young J,  Bandman O,  Hillman JL,  Kaser MR,  Tang YT;
XX
DR   WPI; 1999-457916/38.
DR   N-PSDB; AAX89503.
XX
PT   New tumour necrosis factor-R2-like protein - useful in the treatment
PT   of osteogenesis, developmental, reproductive, immunological and
PT   neoplastic disorders
XX
PS   Claim 1; Fig 1A-C; 81pp; English.
XX
CC   The present sequence represents a human tumour necrosis factor-R2-like
CC   protein (TR2P). The protein is used to treat and prevent osteogenesis,
CC   developmental, reproductive, immunological and neoplastic disorders, and
CC   also to diagnose disorders associated with TR2 protein expression. Such
CC   disorders include osteogenesis disorders such as achondroplasia and
CC   osteoporosis, developmental disorders such as Cushing's syndrome,
CC   muscular dystrophy, and epilepsy, hereditary neuropathies such as
CC   Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism,
CC   hydrocephalus, seizure disorders such as cerebral palsy and spinal
CC   bifida, congenital glaucoma, cataract, or sensorineural hearing loss,
CC   reproductive disorders such as infertility, ovulatory defects and
CC   endometriosis, autoimmune disorders, ectopic pregnancy and teratogenesis,
CC   disruption of spermatogenesis, immunological disorders such as AIDS,
CC   Addison's disease, allergies, bronchitis, atherssclerosis, diabetes
CC   mellitus, Chron's disease, lupus and irritable bowel syndrome, multiple
CC   sclerosis, viral, fungal, helminthic, parasitic and protozoal infections,
CC   and neoplastic disorders including adenocarcinoma, leukaemia, lymphoma,
CC   melanoma, myeloma, sarcoma, and teratocarcinoma.
XX
SQ   Sequence   245 AA;

  Query Match             83.4%;  Score 1362;  DB 20;  Length 245;
  Best Local Similarity   99.6%;  Pred. No. 4e-100;
  Matches  244;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLLQALEAPE 240

Qy        241 GWGPT 245
              |||||
Db        241 DWGPT 245


RESULT 70
AAB28560
ID   AAB28560 standard; protein; 211 AA.
XX
AC   AAB28560;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human soluble TNF receptor tnfrGT-2.
XX
KW   Human; tumour necrosis factor like-1; TNFL1; tumour necrosis factor; TNF;
KW   immunosuppressive; antiarthritic; neuroprotective; dermatalogical;
KW   antiinflammatory; antidiabetic; cytostatic; osteopathic; gene therapy;
KW   colon cancer; rheumatoid arthritis; septic shock; Crohn's disease;
KW   osteoporosis; autoimmune disease; myasthenia gravis;
KW   insulin-dependent diabetes mellitus.
XX
OS   Homo sapiens.
XX
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PN   WO200060079-A2.
XX
PD   12-OCT-2000.
XX
PF   05-APR-2000; 2000WO-US09058.
XX
PR   05-APR-1999;   99US-0286529.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Tribouley C;
XX
DR   WPI; 2000-665004/64.
XX
PT   Tumor necrosis factor (TNF) and TNF receptor superfamily protein
PT   members TNF-L and TNFR-L, useful for enhancing or decreasing TNF
PT   activities such as inducing cell death and lymphoid organogenesis -
XX
PS   Claim 1; Page 77; 77pp; English.
XX
CC   The present sequence is given in a specification relating to an isolated
CC   human protein designated tumour necrosis factor like-1 (TNFL1). It may be
CC   used to induce cell death in tumours, to induce apoptosis of activated T
CC   cells, to induce inflammation, and to rescue resting T cells from
CC   apoptosis. TNF receptors are used to regulate the function of a TNF
CC   ligand which plays a role in apoptosis, inflammation, differentiation, or
CC   proliferation. Expression of the receptors can also be useful as markers
CC   for cancer, especially for colon cancer. Diseases which can be treated
CC   using ligands and/or receptors of the TNF/TNFR superfamily include
CC   rheumatoid arthritis, cancer, septic shock, Crohn's disease and
CC   osteoporosis. The polynucleotides can be used in gene delivery vehicles,
CC   for the purpose of delivering a mRNA or oligonucleotide, full-length
CC   protein, fusion protein, polypeptide, or ribozyme, or single-chain
CC   antibody, into a cell. The newly identified receptor proteins play
CC   regulatory roles in cell proliferation and/or differentiation. The
CC   receptors can also play a role in the negative regulation of
CC   osteoclastogenesis. Soluble TNFR-like receptors can be useful in the
CC   neutralisation of TNF or TNF-like ligands. A TNF-L protein can also be
CC   used to treat autoimmune diseases (myasthenia gravis and
CC   insulin-dependent diabetes mellitus), tumours, and proliferative
CC   disorders. A TNF-L or TNFR-L subgenomic polynucleotide can also be
CC   delivered to subjects for the purpose of screening test compounds for
CC   those which are useful for enhancing transfer of TNF-L subgenomic
CC   polynucleotides to the cell or for enhancing subsequent biological
CC   effects of TNF-L or TNFR-L subgenomic polynucleotides within the cell.
XX
SQ   Sequence   211 AA;

  Query Match             72.0%;  Score 1177;  DB 21;  Length 211;
  Best Local Similarity   99.0%;  Pred. No. 1.5e-85;
  Matches  208;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRALEGPGLSLLCLVLALPALLPVPAVRGVAETPTYPWRDAETGERLVCAQCPPGTFVQR 60

Qy         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PCRRDSPTTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF 120

Qy        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA 180

Qy        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGAEE 210
              |||||||||||||||||||||||||||| |
Db        181 LNVPGSSSHDTLCTSCTGFPLSTRVPGEPE 210


RESULT 71
AAW93585
ID   AAW93585 standard; Protein; 215 AA.
XX
AC   AAW93585;
XX
DT   18-JUN-1999  (first entry)
XX
DE   Human hAPO6 protein.
XX
KW   Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW   developmental abnormality; gestational abnormalitity; prostate cancer;
KW   APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW   cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW   apoptosis; human.
XX
OS   Homo sapiens.
XX
PN   WO9911791-A2.
XX
PD   11-MAR-1999.
XX
PF   04-SEP-1998;   98WO-US18393.
XX
PR   05-SEP-1997;   97US-0924634.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Chaudhary PM;
XX
DR   WPI; 1999-205191/17.
DR   N-PSDB; AAX23419.
XX
PT   New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT   useful for diagnosis and treatment of prostate cancer and
PT   developmental or gestational abnormalities
XX
PS   Claim 29; Fig 9; 156pp; English.
XX
CC   This invention describes isolated Tumor Necrosis Factor (TNF) family
CC   receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC   fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC   their active fragments. APO4 is useful for diagnosing prostate cancer
CC   by determining levels of APO4 in an individual. Prostate cancer can also
CC   be treated using APO4 selective binding agents linked to a therapeutic
CC   moiety. APO4 polypeptides are also useful for identifying selective
CC   binding agents, useful in diagnosis/treatment of disease by binding of
CC   agents to the polypeptide/active fragment which is extracellular, or
CC   expressed on the cell surface. The binding is preferably performed in
CC   vivo. APO4 polypeptides/ active fragments are also useful for screening
CC   for agonists and antagonists by binding and observing the changer in APO4
CC   activity. Effective pharmacological agents useful in diagnosis or
CC   treatment of disease are also identified using APO4 polypeptides/active
CC   fragments and APO4 signal transducer molecules that specifically interact
CC   with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC   activity. The method is performed in vivo or in vitro. APO polypeptides
CC   are all useful as immunogens for preparing antibodies. APO4 is also
CC   useful for diagnosis/treatment of developmental or gestational
CC   abnormalities. APO8 was transfected to human breast carcinoma cell line
CC   MCF-7, and induced apoptosis.
XX
SQ   Sequence   215 AA;

  Query Match             70.6%;  Score 1153;  DB 20;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-83;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         86 ERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPS 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPS 60

Qy        146 QNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRV 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTRV 120

Qy        206 PGAEECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELL 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 PGAEECERAVIDFVAFQDISIKRLQRLLQALEAPEGWGPTPRAGRAALQLKLRRRLTELL 180

Qy        266 GAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 300
              ||||||||||||||||||||||||||||||||||
Db        181 GAQDGALLVRLLQALRVARMPGLERSVRERFLPVH 215


RESULT 72
AAY22222
ID   AAY22222 standard; Protein; 153 AA.
XX
AC   AAY22222;
XX
DT   16-SEP-1999  (first entry)
XX
DE   Human TNFR superfamily soluble receptor protein sequence.
XX
KW   TNFL1; human; TNFR superfamily; tumour necrosis factor ligand; TNF;
KW   tumour necrosis factor receptor; TNFR superfamily; cell proliferation;
KW   cell differentiation; cytokine production; immunoglobulin; hyperplasia;
KW   apoptosis inducer; activated T cell; autoimmune disease; inhibitor;
KW   myasthenia gravis; insulin-dependent diabetes mellitus; endotoxic shock;
KW   rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
KW   tumour; proliferative disorder; neoplasia; dysplasia; immunocompetence;
KW   lymphoid organogenesis; bacterial resistance; contact hypersensitivity;
KW   delayed type sensitivity; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9933980-A2.
XX
PD   08-JUL-1999.
XX
PF   22-DEC-1998;   98WO-US27474.
XX
PR   16-DEC-1998;   98US-0212270.
PR   30-DEC-1997;   97US-0068959.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Kassam A,  Lamson G,  Pot D,  Tribouley C;
XX
DR   WPI; 1999-405508/34.
DR   N-PSDB; AAX84621.
XX
PT   New tumour necrosis factor ligands, useful for induction of cell
PT   death and/or proliferation of cells
XX
PS   Claim 1; Page 61; 69pp; English.
XX
CC   This sequence represents a tumour necrosis factor receptor (TNFR)
CC   superfamily soluble protein of the invention. The invention also relates
CC   to tumour necrosis factor (TNF) ligand (TNFL) family proteins. The TNFL
CC   proteins play regulatory roles in cell proliferation and/or
CC   differentiation, e.g. they can induce production of cytokines,
CC   immunoglobulins, etc. A variety of diseases can be treated by modulating
CC   the activity of TNFL proteins, e.g. they can induce apoptosis of
CC   activated T cells but rescue resting T cell from apoptosis. TNFL
CC   polypeptides can therefore be used to treat autoimmune diseases, such as
CC   myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid
CC   arthritis, multiple sclerosis, and systemic lupus erythematosus. TNFL
CC   proteins also have tumour stimulating properties, so tumours can be
CC   treated by inhibiting the expression or activity of TNFL. Other
CC   proliferative disorders, such as neoplasias, dysplasias, and hyperplasia
CC   can also be treated using TNFL inhibitors. The TNFL polypeptides and
CC   polynucleotides can also be used to enhance or decrease TNF activity,
CC   thus providing therapeutic benefits such as induction of cell death,
CC   lymphoid organogenesis, or host bacterial resistance, and inhibition of
CC   endotoxic shock, contact hypersensitivity, delayed type sensitivity or
CC   immunocompetence of a transplant recipient. TNF and its receptors play a
CC   major role in host defence and immunosurveillance. As such, there is a
CC   need to identify new members of TNFR families. This invention provides
CC   this need.
XX
SQ   Sequence   153 AA;

  Query Match             51.5%;  Score 841;  DB 20;  Length 153;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-59;
  Matches  153;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         85 LERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTP 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTP 60

Qy        145 SQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTR 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTR 120

Qy        205 VPGAEECERAVIDFVAFQDISIKRLQRLLQALE 237
              |||||||||||||||||||||||||||||||||
Db        121 VPGAEECERAVIDFVAFQDISIKRLQRLLQALE 153


RESULT 73
AAB28554
ID   AAB28554 standard; protein; 153 AA.
XX
AC   AAB28554;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human TNFR soluble receptor #1.
XX
KW   Human; tumour necrosis factor like-1; TNFL1; tumour necrosis factor; TNF;
KW   immunosuppressive; antiarthritic; neuroprotective; dermatalogical;
KW   antiinflammatory; antidiabetic; cytostatic; osteopathic; gene therapy;
KW   colon cancer; rheumatoid arthritis; septic shock; Crohn's disease;
KW   osteoporosis; autoimmune disease; myasthenia gravis;
KW   insulin-dependent diabetes mellitus.
XX
OS   Homo sapiens.
XX
PN   WO200060079-A2.
XX
PD   12-OCT-2000.
XX
PF   05-APR-2000; 2000WO-US09058.
XX
PR   05-APR-1999;   99US-0286529.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Tribouley C;
XX
DR   WPI; 2000-665004/64.
DR   N-PSDB; AAC63757.
XX
PT   Tumor necrosis factor (TNF) and TNF receptor superfamily protein
PT   members TNF-L and TNFR-L, useful for enhancing or decreasing TNF
PT   activities such as inducing cell death and lymphoid organogenesis
XX
PS   Claim 1; Page 65; 77pp; English.
XX
CC   The present sequence is given in a specification relating to an isolated
CC   human protein designated tumour necrosis factor like-1 (TNFL1). It may be
CC   used to induce cell death in tumours, to induce apoptosis of activated T
CC   cells, to induce inflammation, and to rescue resting T cells from
CC   apoptosis. TNF receptors are used to regulate the function of a TNF
CC   ligand which plays a role in apoptosis, inflammation, differentiation, or
CC   proliferation. Expression of the receptors can also be useful as markers
CC   for cancer, especially for colon cancer. Diseases which can be treated
CC   using ligands and/or receptors of the TNF/TNFR superfamily include
CC   rheumatoid arthritis, cancer, septic shock, Crohn's disease and
CC   osteoporosis. The polynucleotides can be used in gene delivery vehicles,
CC   for the purpose of delivering a mRNA or oligonucleotide, full-length
CC   protein, fusion protein, polypeptide, or ribozyme, or single-chain
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CC antibody, into a cell. The newly identified receptor proteins play
CC regulatory roles in cell proliferation and/or differentiation. The
CC receptors can also play a role in the negative regulation of
CC osteoclastogenesis. Soluble TNFR-like receptors can be useful in the
CC neutralisation of TNF or TNF-like ligands. A TNF-L protein can also be
CC used to treat autoimmune diseases (myasthenia gravis and
CC insulin-dependent diabetes mellitus), tumours, and proliferative
CC disorders. A TNF-L or TNFR-L subgenomic polynucleotide can also be
CC delivered to subjects for the purpose of screening test compounds for
CC those which are useful for enhancing transfer of TNF-L subgenomic
CC polynucleotides to the cell or for enhancing subsequent biological
CC effects of TNF-L or TNFR-L subgenomic polynucleotides within the cell.
XX
SQ Sequence 153 AA;

Query Match 51.5%; Score 841; DB 21; Length 153;
Best Local Similarity 100.0%; Pred. No. 4.4e-59;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        85 LERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTP 144
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Db         1 LERCRYCNVLCGEREEEARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTP 60

Qy       145 SQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTR 204
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 SQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLALNVPGSSSHDTLCTSCTGFPLSTR 120

Qy       205 VPGAEECERAVIDFVAFQDISIKRLQRLLQALE 237
             |||||||||||||||||||||||||||||||||
Db       121 VPGAEECERAVIDFVAFQDISIKRLQRLLQALE 153
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